


IN THE UNITED STATES PATENT AND TRADEMARK OFFICE



Applicant : Eaton, et al.
Appl. No. : 10/063,557
Filed : May 2, 2002
For : SECRETED AND
TRANSMEMBRANE
POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
Examiner : David J. Blanchard
Group Art Unit : 1642

DECLARATION OF J. CHRISTOPHER GRIMALDI, UNDER 37 CFR §1.132

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I, J. Christopher Grimaldi, declare and state as follows:

1. I am a Senior Research Associate in the Molecular Biology Department of Genentech, Inc., South San Francisco, CA 94080.
2. My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).
3. I joined Genentech in January of 1999. From 1999 to 2003, I directed the Cloning Laboratory in the Molecular Biology Department. During this time I directed or performed numerous molecular biology techniques including semi-quantitative Polymerase Chain Reaction (PCR) analyses. I am currently involved, among other projects, in the isolation of genes coding for membrane associated proteins which can be used as targets for antibody therapeutics against cancer. In connection with the above-identified patent application, I personally performed or directed the semi-quantitative PCR gene expression analyses in the assay entitled "Tumor Versus Normal Differential Tissue Expression Distribution," which is described in EXAMPLE 18 in the specification. These studies were used to identify differences in gene expression between tumor tissue and their normal counterparts.
4. EXAMPLE 18 reports the results of the PCR analyses conducted as part of the investigating of several newly discovered DNA sequences. This process included developing

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primers and analyzing expression of the DNA sequences of interest in normal and tumor tissues. The analyses were designed to determine whether a difference exists between gene expression in normal tissues as compared to tumor in the same tissue type.

5. The DNA libraries used in the gene expression studies were made from pooled samples of normal and of tumor tissues. Data from pooled samples is more likely to be accurate than data obtained from a sample from a single individual. That is, the detection of variations in gene expression is likely to represent a more generally relevant condition when pooled samples from normal tissues are compared with pooled samples from tumors in the same tissue type.

6. In differential gene expression studies, one looks for genes whose expression levels differ significantly under different conditions, for example, in normal versus diseased tissue. Thus, I conducted a semi-quantitative analysis of the expression of the DNA sequences of interest in normal versus tumor tissues. Expression levels were graded according to a scale of +, -, and +/- to indicate the amount of the specific signal detected. Using the widely accepted technique of PCR, it was determined whether the polynucleotides tested were more highly expressed, less expressed, or whether expression remained the same in tumor tissue as compared to its normal counterpart. Because this technique relies on the visual detection of ethidium bromide staining of PCR products on agarose gels, it is reasonable to assume that any detectable differences seen between two samples will represent at least a two fold difference in cDNA.

7. The results of the gene expression studies indicate that the genes of interest can be used to differentiate tumor from normal. The precise levels of gene expression are irrelevant; what matters is that there is a relative difference in expression between normal tissue and tumor tissue. The precise type of tumor is also irrelevant; again, the assay was designed to indicate whether a difference exists between normal tissue and tumor tissue of the same type. If a difference is detected, this indicates that the gene and its corresponding polypeptide and antibodies against the polypeptide are useful for diagnostic purposes, to screen samples to differentiate between normal and tumor. Additional studies can then be conducted if further information is desired.

8. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By:

J Christopher Grimaldi

Date:

8/10/2004

J. Christopher Grimaldi

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San Francisco, CA 94122
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EDUCATION

University of California, Berkeley
Bachelor of Arts in Molecular Biology, 1984

EMPLOYMENT EXPERIENCE

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3. My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).
4. In differential gene expression studies, one looks for genes whose expression levels differ significantly under different conditions, for example, in normal versus diseased tissue.

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Chromosomal aberrations, such as gene amplification, and chromosomal translocations are important markers of specific types of cancer and lead to the aberrant expression of specific genes and their encoded polypeptides, including over-expression and under-expression. For example, gene amplification is a process in which specific regions of a chromosome are duplicated, thus creating multiple copies of certain genes that normally exist as a single copy. Gene under-expression can occur when a gene is not transcribed into mRNA. In addition, chromosomal translocations occur when two different chromosomes break and are rejoined to each other chromosome resulting in a chimeric chromosome which displays a different expression pattern relative to the parent chromosomes. Amplification of certain genes such as Her2/Neu [Singleton *et al.*, Pathol. Annu., 27Pt1:165-190], or chromosomal translocations such as t(5;14), [Grimaldi *et al.*, Blood, 73(8):2081-2085(1989); Meeker *et al.*, Blood, 76(2):285-289(1990)] give cancer cells a growth or survival advantage relative to normal cells, and might also provide a mechanism of tumor cell resistance to chemotherapy or radiotherapy. When the chromosomal aberration results in the aberrant expression of a mRNA and the corresponding gene product (the polypeptide), as it does in the aforementioned cases, the gene product is a promising target for cancer therapy, for example, by the therapeutic antibody approach.

5. Comparison of gene expression levels in normal versus diseased tissue has important implications both diagnostically and therapeutically. For example, those who work in this field are well aware that in the vast majority of cases, when a gene is over-expressed, as evidenced by an increased production of mRNA, the gene product or polypeptide will also be over-expressed. It is unlikely that one identifies increased mRNA expression without associated increased protein expression. This same principle applies to gene under-expression. When a gene is under-expressed, the gene product is also likely to be under-expressed. Stated in another way, two cell samples which have differing mRNA concentrations for a specific gene are expected to have correspondingly different concentration of protein for that gene. Techniques used to detect mRNA, such as Northern Blotting, Differential Display, *in situ* hybridization, quantitative PCR, Taqman, and more recently Microarray technology all rely on the dogma that a change in mRNA will represent a similar change in protein. If this dogma did not hold true then these techniques would have little value and not be so widely used. The use of mRNA quantitation techniques have identified a seemingly endless number of genes which are differentially expressed in various tissues and these genes have subsequently been shown to have correspondingly similar changes in their protein levels. Thus, the detection of increased mRNA expression is expected to result in increased polypeptide expression, and the detection of decreased mRNA expression is expected to result in decreased polypeptide expression. The detection of increased or decreased polypeptide expression can be used for cancer diagnosis and treatment.

6. However, even in the rare case where the protein expression does not correlate with the mRNA expression, this still provides significant information useful for cancer diagnosis and treatment. For example, if over- or under-expression of a gene product does not correlate with over- or under-expression of mRNA in certain tumor types but does so in others, then identification of both gene expression and protein expression enables more accurate tumor classification and hence better determination of suitable therapy. In addition, absence of over- or

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under-expression of the gene product in the presence of a particular over- or under-expression of mRNA is crucial information for the practicing clinician. For example, if a gene is over-expressed but the corresponding gene product is not significantly over-expressed, the clinician accordingly will decide not to treat a patient with agents that target that gene product.

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

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071904

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 Biological Safety Affairs Forum (BSAF) 1990-1991
 Environmental Law Foundation (ELF) 1990-1991

The t(5;14) Chromosomal Translocation in a Case of Acute Lymphocytic Leukemia Joins the Interleukin-3 Gene to the Immunoglobulin Heavy Chain Gene

By J. Christopher Grimaldi and Timothy C. Meeker

Chromosomal translocations have proven to be important markers of the genetic abnormalities central to the pathogenesis of cancer. By cloning chromosomal breakpoints one can identify activated proto-oncogenes. We have studied a case of B-lineage acute lymphocytic leukemia (ALL) that was associated with peripheral blood eosinophilia. The chromosomal translocation t(5;14) (q31;q32) from this sample was cloned and studied at the molecular level. This

translocation joined the immunoglobulin heavy chain joining (Jh) region to the promoter region of the interleukin-3 (IL-3) gene in opposite transcriptional orientations. The data suggest that activation of the IL-3 gene by the enhancer of the immunoglobulin heavy chain gene may play a central role in the pathogenesis of this leukemia and the associated eosinophilia.

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KARYOTYPIC STUDIES of leukemia and lymphoma have identified frequent nonrandom chromosomal translocations. Some of these translocations juxtapose the immunoglobulin heavy chain (IgH) gene with important

protooncogenes, such as *c-myc* and *bcl-2*.^{1,2} In this way, the IgH gene can activate proto-oncogenes, resulting in disordered gene expression and a step in the development of cancer. The investigation of additional nonrandom translocations into the IgH locus allows us to identify new genes promoting the generation of leukemia and lymphoma.

A distinct subtype of acute lymphocytic leukemia (ALL) has been characterized by B-lineage phenotype, associated eosinophilia in the peripheral blood, and a t(5;14)(q31;q32) chromosomal translocation.^{3,4} This syndrome probably occurs in <1% of all patients with ALL. We hypothesized that the cloning of the translocation characteristic of this leukemia might allow the identification of an important gene on chromosome 5 that plays a role in the evolution of this disease. In this report we demonstrate that the interleukin-3 gene (IL-3) and the IgH gene are joined by this translocation.

MATERIALS AND METHODS

Sample and DNA blots. A bone marrow aspirate from a representative patient with ALL (L1 morphology by French-American-British [FAB] criteria), peripheral eosinophilia (up to 20,000 per microliter with a normal value of <350 per microliter) and a t(5;14)(q31;q32) translocation was studied. Using published methods, genomic DNA was isolated and DNA blots were made.⁵ Briefly, 10 µg of high molecular weight (mol wt) DNA were digested using an appropriate restriction enzyme and electrophoresed on a 0.8% agarose gel. The gel was stained with ethidium bromide, photographed, denatured, neutralized, and transferred to Hybond (Amersham, Arlington Heights, IL). After treatment of the filter with ultraviolet light, hybridization was performed. The filter was washed to a final stringency of 0.2% saturated sodium citrate (SSC) and 0.1% sodium lauryl sulfate (SDS) and exposed to film. The human Jh probe has been previously reported.⁶

Genomic library. The genomic library was made using pub-

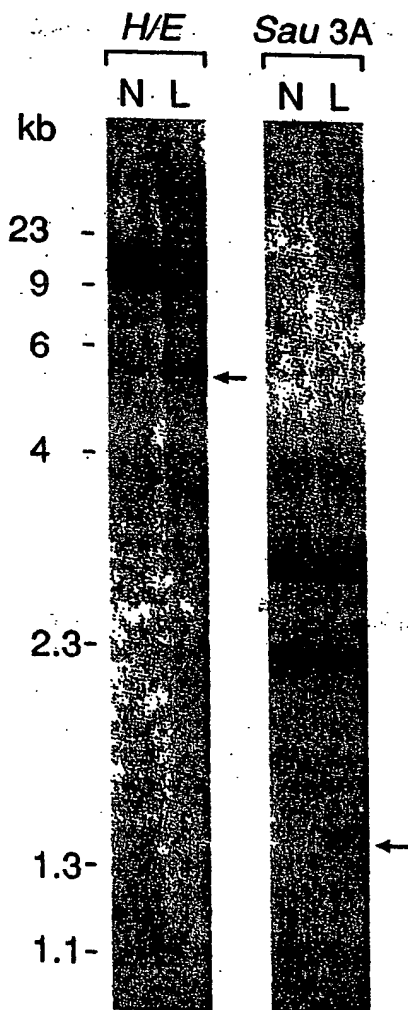


Fig 1. DNA blots of the leukemia sample. The restriction fragment pattern of normal human DNA (N) and the leukemia sample (L) were compared using a human Jh probe. Rearranged bands are indicated by arrows. Sample L exhibits a single rearranged band with both *Hind* III/*Eco*RI and *Sau*3A restriction digests. The rearranged bands are less intense than the other bands because the majority of cells in the sample represent normal bone marrow elements.

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lished methods.⁵ Approximately 100 μ g of high mol wt genomic DNA were partially digested with the *Sau*3A restriction enzyme. Fragments from 9 to 23 kilobases (kb) in size were isolated on a sucrose gradient and ligated into phage EMBL3A (Stratagene, San Diego). Recombinant phage were packaged, plated, and screened as previously reported.⁵

DNA sequencing. Fragments for sequencing were cloned into M13 vectors and sequenced by the chain termination method using Sequenase (United States Biochemical, Cleveland).⁷ All sequence data were derived from both strands.

RESULTS

We studied a bone marrow sample from a patient with ALL and associated peripheral eosinophilia. Karyotypic analysis showed the characteristic t(5;14)(q31;q32) translocation. These features define a distinctive subtype of ALL.^{3,4} The leukemic cells were analyzed for cell surface phenotype by immunofluorescence. They were positive for B1 (CD20), B4 (CD19), cALLA (CD10), HLA-DR, and terminal deoxynucleotidyl transferase (Tdt), but negative for surface immunoglobulin. This phenotypic profile describes an immature cell from the B-lymphocytic lineage.⁸

The leukemia DNA was analyzed by Southern blotting for rearrangements of the IgH gene. Using a human immunoglobulin Jh probe, a single rearranged band was detected by *Eco*RI, *Hind*III, *Sst*I, *Sau*3A, and *Eco*RI plus *Hind*III restriction digests, suggesting rearrangement of one allele (Fig 1). The immunoglobulin Jh region from the other allele was presumably either deleted or in the germline configuration.

We hypothesized that the t(5;14)(q31;q32) juxtaposed a

growth-promoting gene on chromosome 5 with the immunoglobulin Jh region on chromosome 14. Therefore, a genomic library was made from the leukemic sample and screened with a Jh probe. Fifteen distinct positive clones were isolated and screened for the presence of the rearranged *Sau*3A fragment that was detected by DNA blotting. By this analysis, five clones appeared to represent the rearranged allele identified by DNA blots. One of these clones (clone no. 4) was chosen for further study and a detailed restriction map was generated. The *Eco*RI, *Hind*III/*Eco*RI, and *Sst*I fragments from clone no. 4 that hybridized to the human Jh probe were also identical in size to the rearranged fragments from the leukemia sample, confirming that clone no. 4 represented the rearranged leukemic allele.

Phage clone no. 4 contained 3.7 kb of unknown origin joined to the IgH gene in the region of Jh4 (Fig 2). The IgH gene from Jh4 to the Cmu region appeared to be in germline configuration. Previously, the gene encoding hematopoietic growth factor IL-3 had been mapped to chromosome 5q31 so it was suspected that clone no. 4 might contain part of this gene.⁹⁻¹² When the restriction map of human IL-3 and clone no. 4 were compared, they were identical for more than 3 kb (Fig 2).

We confirmed the juxtaposition of the IL-3 gene and the IgH gene by nucleic acid sequencing of the subcloned *Bst*EII/*Hpa*I fragment (Fig 2). The sequence of this fragment showed no disruption of the protein coding region or the messenger RNA of the IL-3 gene. The break in the IL-3 gene occurred in the promoter region, 452 base pairs (bp) upstream of the transcriptional start site (position 64, Fig

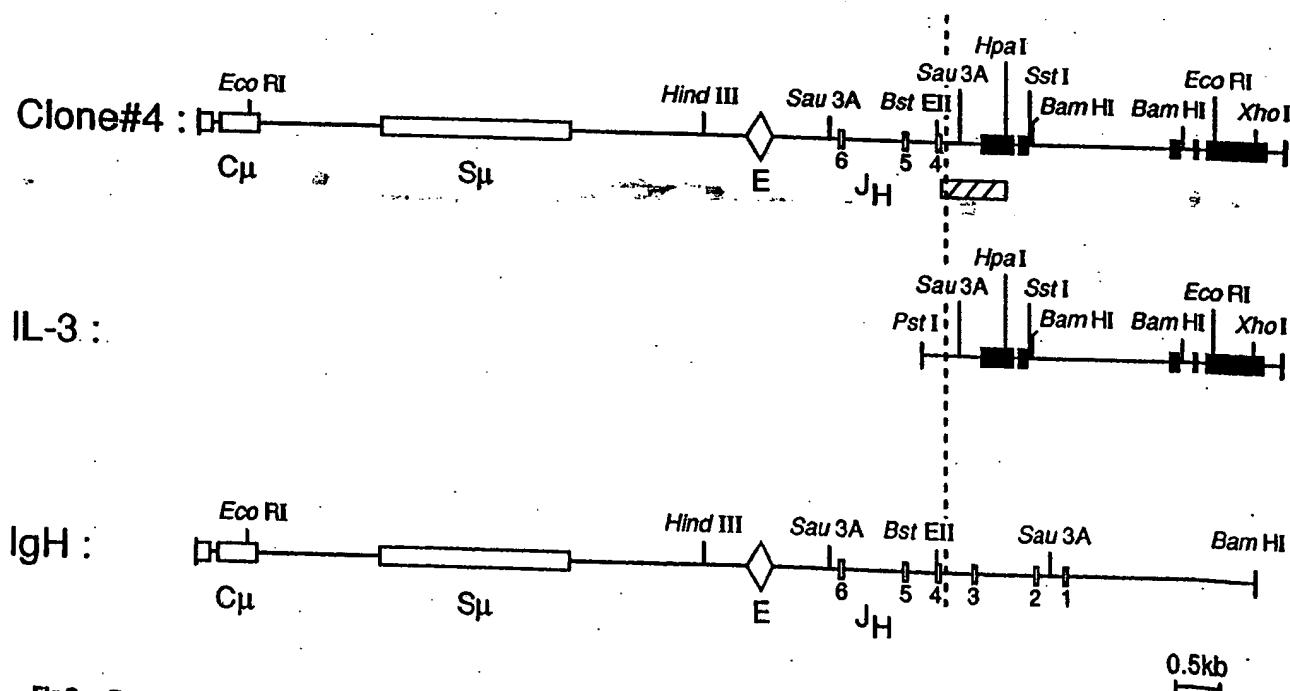


Fig 2. Breakpoint region: t(5;14)(q31;q32). Comparative mapping of phage clone no. 4, the germline IgH region, and the germline IL-3 gene.^{23,29} The map of clone no. 4 is identical to that of IgH until it diverges in the region of Jh4 (at the dashed line), after which it is identical to the map of IL-3. The two genes are positioned in a head-to-head orientation. The Ig μ chain constant region (C μ), switch region (S μ), and Jh segments are indicated (open symbols). The five exons (dark boxes) and four introns of the IL-3 gene are shown. The hatched box indicates the sequenced region.

3A). The break in the IgH gene occurred 2 bp upstream of the Jh4 region. Between the two breaks, 25 bp of uncertain origin (putative N sequence) were inserted.^{13,14} No sequences homologous to the immunoglobulin heptamer and nonamer could be identified in the IL-3 sequence (Fig 3B). Therefore, nucleic acid sequencing confirmed the juxtaposition of the IL-3 gene and the IgH gene. The sequence data clearly showed that the genes were positioned in opposite transcriptional orientations (head-to-head).

Available data also allowed us to determine the normal positions of the IL-3 gene and the GM-CSF gene in relation to the centromere of chromosome 5 (Fig 4). The IgH gene is known to be positioned with the variable regions toward the telomere on chromosome 14q.^{2,15} It has also been shown that

GM-CSF maps within 9 kb of IL-3 in the same transcriptional orientation.¹⁶ Using this information and assuming a simple translocation event in our sample, we can conclude that the IL-3 gene is normally more centromeric, and the GM-CSF gene more telomeric on chromosome 5q (Fig 4). Furthermore, both are transcribed with their 5' ends toward the centromere.

DISCUSSION

In this report we have cloned a unique chromosomal translocation that appears to be a consistent feature of a rare, yet distinct, clinical form of acute leukemia. This translocation joined the promoter of the IL-3 gene to the IgH gene. Except for the altered promoter, the IL-3 gene appeared

A

5' GGTGACCAGGGTTCCTGGCCCCAGTAGTCAAAGTAGTAGAGTAATTCATCATAGCTGCGGATTAGCAGCGTGACCGGC 80
 3' CCACTGGTCCCAAGGGACCGGGTCATCAGTTTCATCATCTCCATTAAGTAGTATCGACGCCAATCGTCGCACTGCGCG

5' TACCAGACAAACTCTCATCTGTTCCAGTGGCCTCTGGCCACCCACCAGGACCAAGCAGGGCGGGCAGCAGAGGGCCAGG 160
 3' ATGGTCTGTTTGAGAGTAGACAAGGTCACCGGAGGACCGGTGGTGGTCTGCTCGTCCCGCCCGTCGTCTCCCGGTCC

5' GTAGTCCAGGTGATGGCAGATGAGATCCCACTGGGCAGGAGGCCTCAGTGAGCTGAGTCAGGCTTCCCTTCTCTGCCACA 240
 3' CATCAGGTCCACTACCGTCTACTCTAGGGTGACCGCTCTCCGGAGTCACTCGACTCAGTCCGAAGGGGAAGGACGGTGT

5' GGGGTCTCTCACCTGCTGCCATGCTTCCCATCTCTCATCTCTCTGACAAGATGAAGTGATACCGTTTAAGTAATCTTT 320
 3' CCCAGGAGAGTGGACGACGGTACGAAGGGTAGAGAGTAGGAGGAAGTGTCTACTTCACTATGGCAAATTCATTAGAAA

5' TTCTTGTGTTCACTGATCTGAGTACTAGAAAGTCATGGATGAATAATTACGCTCTGTGGTTTCTATGGAGGTTCATGT 400
 3' AAAGAACAAGTGACTAGAACTCATGATCTTTCACTACCTACTTATTAATGCAGACACCAAAAGATACCTCCAAGGTACA

5' CAGATAAAGATCCTTCCGACGCTGCCCCACACCACCCTCCCCCGCCTTGCCCCGGGGTGTGGGCACCTTGCTGCTG 480
 3' GTCTATTCTAGGAAGGCTGCGGACGGGTGTGGTGGTGAGGGGGGGCGGAACGGGCCCCAACACCCGTGGAACGACGAC

5' CACATATAAGGCGGGAGGTGTGTCCTCACTCTTCAGAGCCCCACGAAGGACCAGAACAAGACAGAGTGCCCTCTGCCGAT 560
 3' GTGTATATTCGCCCTCCAACAACGGTTGAGAAGTCTCGGGGTGCTTCTGCTTGTCTGTCTACGGAGGACGGCTA

5' CCAACATGAGCCGCTGCCCGTCTGCTCCTCACTCTGGTCCGCCCGGACTCCAAGCTCCCATGACCCAGAC 640
 3' GGTGTGACTCGGCGGACGGGCAGGACGAGGACGAGGTTGAGGACAGGCGGGGCTGAGGTTGAGGGTACTGGGTCTG

5' AACGTCCTTGAAGACAAGCTGGGTAAAC 3' 668
 3' TTGCAGGAACCTTCTGTTCGACCCAATTG 5'

B

IgJh4 5' TGGCCCCAGTAGTCAAAGTAGTCACATTGTGGGAGGCCCATTAAGGGGTGCACAAAACCTGACTCTC
 3' ACCGGGGTCATCAGTTTCATCAGTGTAACACCCCTCCGGGGTAATTCACCGTGTGTTTGGACTGAGAG
 ++++++

Cl.#4 5' TGGCCCCAGTAGTCAAAGTAGTAGAGTAATTCATCATAGCTGCGGATTAGCAGCGTGACCGGCTACCA
 3' ACCGGGGTCATCAGTTTCATCATCTCCATTAAGTAGTATCGACGCCAATCGTCGCACTGGCCGATGGT
 ++++++

IL-3 5' GGCACCAAGAGATGTGCTTCTCAGAGCCTGAGGCTGAACGTGGATGTTTAGCAGCGTGACCGGCTACCA
 3' CCGTGGTTCCTACACGAAGAGTCTCGGACTCCGACTGCACCTACAAATCGTCGCACTGGCCGATGGT

Fig 3. Sequence of t(5;14)(q31;q32) breakpoint region. (A) Nucleotide sequence of the *Bst*II/*Hpa*I fragment indicated on Fig 2. Nucleotides 1 to 36 represent the Jh4 coding region underlined on the coding strand.⁸ Nucleotides 39 to 63 are a putative N region. The sequence from position 64 to 668 is that of the germline IL-3 gene.²⁰ The IL-3 TATA box (486), transcription start (516), and initiation methionine (567) are underlined. Two proposed regulatory sequences in the promoter are marked by asterisks (positions 182 and 389). (B) Comparative sequence of the t(5;14)(q31;q32) breakpoint region. The IgJh4 region is shown with its coding region, heptamer, and nonamer underlined. Clone no. 4 is shown with putative N region sequences underlined. The IL-3 sequence is also shown. A plus sign (+) denotes the identical nucleotide between sequences. No heptamer or nonamer is identified in the IL-3 sequence.

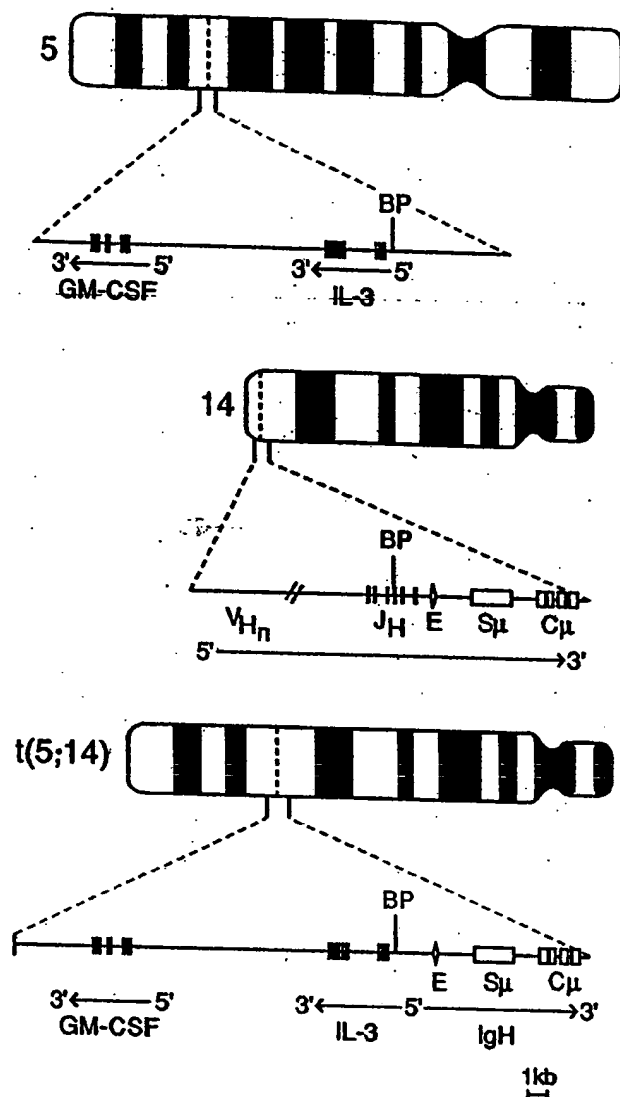


Fig 4. Diagram of the translocation. The normal chromosome 5q31 is shown with the GM-CSF gene telomeric to the IL-3 gene in the transcriptional orientation shown. On normal chromosome 14q32 the V_H regions are telomeric. The t(5;14)(q31;q32) translocation results in the head-to-head orientation of these genes. Symbols are defined in Fig 2. BP, breakpoint position.

intact as no deletions, insertions, or point mutations were detected by restriction mapping of the entire gene and sequencing of part of the gene. The IgH gene has been truncated at the Jh4 region, which places the immunoglobulin enhancer within 2.5 kb of the IL-3 gene.^{17,18} This leads to the hypothesis that the enhancer is increasing transcription of a structurally normal IL-3 gene. The same mechanism is important for activation of the *c-myc* gene in some cases of Burkitt's lymphoma.¹⁹ An alternate hypothesis is that the elimination of an upstream IL-3 promoter element is crucial to the activation of the IL-3 gene.

The proposed activation of the IL-3 gene suggests that an autocrine loop is important for the pathogenesis of this leukemia.²⁰ Over-expression of the IL-3 gene coupled with

the presence of the IL-3 receptor in these cells could account for a strong stimulus for proliferation. In this regard, there are data indicating that immature B-lineage lymphocytes and B-lineage leukemias may express the IL-3 receptor.^{21,22}

An additional feature of this type of leukemia is the dramatic eosinophilia, consisting of mature forms. It has been hypothesized that the eosinophils do not arise from the malignant clone, but are stimulated by the tumor.^{23,24} Because of the known effect of IL-3 on eosinophil differentiation, secretion of high levels of IL-3 by leukemic cells might have a role in the eosinophilia in this type of leukemia.¹²

The data suggest that the recombination mechanism that is active in the IgH gene during normal differentiation has a role in this translocation.^{13,14} This is supported by the breakpoint location at the 5' end of Jh4 and the presence of putative N-region sequences. On the other hand, no recombination signal sequence (heptamer and nonamer) was found in this region on chromosome 5, suggesting that additional factors also played a role. Further studies will elucidate the mechanism of this and other translocations.

In the leukemia we studied, it is possible that the immunoglobulin enhancer also activates the GM-CSF gene, since this gene is probably positioned only 14 kb away (Fig 4). This is known to be within the range of enhancer activation.²⁵ The interleukin-5 (IL-5) gene maps to chromosome 5q31.²⁶ Deregulation of the IL-5 gene by this translocation would act synergistically with IL-3 in the stimulation of eosinophil proliferation and differentiation.²⁷ These and other questions will be answered by the study of more patient samples. We plan to determine whether the t(5;14)(q31;q32) translocation is capable of activating multiple lymphokines simultaneously and whether they cooperate in the generation of this leukemia.

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RAPID COMMUNICATION

Activation of the Interleukin-3 Gene by Chromosome Translocation in Acute Lymphocytic Leukemia With Eosinophilia

By Timothy C. Meeker, Dan Hardy, Cheryl Willman, Thomas Hogan, and John Abrams

The t(5;14)(q31;q32) translocation from B-lineage acute lymphocytic leukemia with eosinophilia has been cloned from two leukemia samples. In both cases, this translocation joined the IgH gene and the interleukin-3 (IL-3) gene. In one patient, excess IL-3 mRNA was produced by the leukemic cells. In the second patient, serum IL-3 levels were measured and shown to correlate with disease

activity. There was no evidence of excess granulocyte/macrophage colony stimulating factor (GM-CSF) or IL-5 expression. Our data support the formulation that this subtype of leukemia may arise in part because of a chromosome translocation that activates the IL-3 gene, resulting in autocrine and paracrine growth effects.

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A NUMBER OF chromosome translocations have been associated with human leukemia and lymphoma. In many cases the study of these translocations has led to the discovery or characterization of proto-oncogenes, such as *bcl-2*, *c-abl*, and *c-myc*, that are located adjacent to the translocation.^{1,2} It is now widely understood that cancer-associated translocations disrupt nearby proto-oncogenes.

A distinct subtype of acute leukemia is characterized by the triad of B-lineage immunophenotype, eosinophilia, and the t(5;14)(q31;q32) translocation.^{3,4} Leukemic cells from such patients have been positive for terminal deoxynucleotidyl transferase (Tdt), common acute lymphoblastic leukemia antigen (CALLA), and CD19, but negative for surface or cytoplasmic immunoglobulin. In previous work, we cloned the t(5;14) breakpoint from one leukemic sample (Case 1) and determined that the IgH and interleukin-3 (IL-3) genes were joined by this abnormality.⁵ In this report, we extend those findings by showing that the t(5;14)(q31;q32) translocation from a second leukemia sample (Case 2) has a similar structure, and we report our study of growth factor expression in these patients.

MATERIALS AND METHODS

Samples and Southern blots. Case 1 has been described.^{5,6} Clinical features of Case 2 have been described in detail.⁷ DNA isolation and Southern blotting was done using previously described methods.⁸ Filters were hybridized with an immunoglobulin Jh probe, a 280 bp *Bam*HI/*Eco*RI genomic IL-3 fragment, and an IL-3 cDNA probe.^{7,8}

Northern blots. RNA isolation and Northern blotting have been described.⁹ Briefly, Northern blots were done by separating 9 µg total RNA on 1% agarose-formaldehyde gels. Equal RNA loading in each lane was confirmed by ethidium bromide staining. Blots were hybridized with an IL-3 cDNA probe extending to the *Xho*I site in exon 5, a 720 bp *Sst*I/*Kpn*I probe derived from intron 2 of the IL-3 gene, a 600 bp *Nhe*I/*Hpa*I IL-5 cDNA probe, and a 500 bp *Pst*I/*Nco*I granulocyte-macrophage colony stimulating factor (GM-CSF) cDNA probe.¹⁰⁻¹²

Polymerase chain reaction. Primers were designed with *Bam*HI sites for cloning. One primer hybridized to the Jh sequences from the IgH gene (Primer 144: 5'-TAGGATCCGACGGTGACCAAGGGT), and the other hybridized to the region of the TATA box in the IL-3 gene (Primer 161: 5'-AACAGGATCCCGCCTTATATGTGCAG). Polymerase chain reaction (PCR) (95°C for 1 minute, 61°C for 30 seconds, and 72°C for 3 minutes) was done using 500 ng genomic DNA and 50 pmol of each primer in 100 µL containing 67 mmol/L Tris-HCl pH 8.8, 6.7 mmol/L MgCl₂, 10% dimethyl sulfoxide (DMSO), 170 µg/mL bovine serum albumin (BSA) (fraction V),

16.6 mmol/L ammonium sulfate, 1.5 mmol/L each dNTP and Taq polymerase (Perkin-Elmer, Norwalk, CT).¹³

Sequencing. Sequencing was done by chain termination in M13 vectors.¹⁴ As part of this study, we sequenced a subclone of a normal IL-3 promoter, covering 598 base pairs from a *Sma*I site at position -1240 (with respect to the proposed site of transcription initiation) to an *Nhe*I site at position -642. The plasmid containing this region was a gift from Naoko Arai of the DNAX Research Institute.

Expression in Cos7 cells. A genomic IL-3 fragment from Case 1 was cloned into the pXM expression vector.¹⁵ Briefly, the *Hind*III/*Sal*I fragment containing the IL-3 gene was subcloned from the previously described phage clone 4 into pUC18.⁵ The 2.6 kb fragment extending from the *Sma*I site 61 bp upstream of the IL-3 transcription start to the *Sma*I site in the polylinker was cloned into the blunted *Xho*I site of pXM. The negative control construct was the pXM vector without insert. Plasmids were introduced into Cos7 cells by electroporation, and supernatant was collected after 48 hours in culture.

TF1 bioassay. TF-1 cells were passaged in RPMI 1640 supplemented with 10% heat-inactivated fetal bovine serum, 2 mmol L-glutamine, and 1 ng/mL human GM-CSF.¹⁶ Samples and antibodies were diluted in this same medium lacking GM-CSF but containing penicillin and streptomycin. A 25 µL volume of serial dilutions of patient serum was added to wells in a flat bottom 96-well microtiter plate. Rat anti-cytokine monoclonal antibody in a volume of 25 µL was added to appropriate wells and preincubated for 1 hour at 37°C. Fifty microliters of twice washed TF-1 cells were added to each well, giving a final cell concentration of 1×10^4 cells per well (final volume, 100 µL). The plate was incubated for 48 hours. The remaining cell viability was determined metabolically by the colori-

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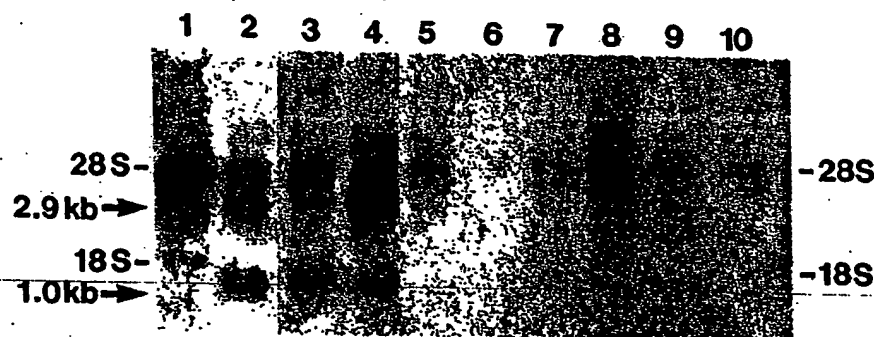


Fig 3. Documentation of IL-3 mRNA over-expression. A Northern blot was prepared and hybridized with a probe for IL-3. Lane 1 contained RNA from unstimulated peripheral blood lymphocytes (PBL) as a negative control. Lane 2 contained RNA from PBL stimulated for 4 hours with concanavalin A (ConA), and lane 3 contained RNA from PBL stimulated with ConA for 48 hours. As in the positive control lanes (2 and 3), a 1 kb band was identified in the leukemic sample from Case 1 (lane 4, lower arrow), suggesting aberrant expression of the IL-3 gene. In addition, the leukemic sample showed over-expression of an unspliced 2.9 kb IL-3 transcript (lane 4, upper arrow). We documented that this represented an unspliced precursor of the mature 1 kb transcript by showing that this band hybridized to a probe from intron 2 of the IL-3 gene. A similar 2.9 kb band was detected in lane 2, suggesting that an IL-3 mRNA of this size is sometimes detectable in normal mitogen-stimulated cells. Lane 5 through 10 represent RNA from six samples of B-lineage acute lymphocytic leukemia without the t(5;14) translocation, indicating that only the sample with the translocation exhibited IL-3 over-expression. Case 2 could not be analyzed by Northern blot because too few cells were available for study.

the locations of the two cloned breakpoints in relation to the IL-3 gene. The two chromosome 5 breakpoints were separated by less than 500 bp.

The genomic structure in Cases 1 and 2 suggested that a normal IL-3 gene product was over-expressed as a result of the altered promoter structure. This would predict that the IL-3 gene on the translocated chromosome was capable of making IL-3 protein. This prediction was tested by expressing a genomic fragment from the translocated allele of Case 1 containing all five IL-3 exons under the control of the SV40 promoter/enhancer in the Cos7 cell line. Cell supernatants were studied in a proliferation assay using the factor dependent erythroleukemic cell line, TF-1. The supernatants derived from transfections using the vector plus insert supported TF-1 proliferation, while supernatants from transfections using the vector alone were negative in this assay (data not shown). Furthermore, the biologic activity could be blocked by an antibody to human IL-3 (BVD3-6G8). This result showed that the translocated allele retained the ability to make IL-3 mRNA and protein.

The level of expression of IL-3 mRNA in leukemic cells from Case 1 was assessed. Northern blotting showed that the mature IL-3 mRNA (approximately 1 kb) and a 2.9 kb unspliced IL-3 mRNA were excessively produced by the leukemia (Fig 3). The 2.9 kb form of the mRNA is also present at low levels in normal peripheral blood T lymphocytes after mitogen activation (Fig 3). Several B-lineage acute leukemia samples without the t(5;14) translocation had undetectable levels of IL-3 mRNA in these experiments. In addition, although genes for GM-CSF and IL-5 map close to the IL-3 gene and might have been deregulated by the translocation, no IL-5 or GM-CSF mRNA could be detected in the leukemic sample (data not shown).^{19,20}

Three serum samples from Case 2 were assayed by immunoassay for levels of IL-3, GM-CSF, and IL-5 (Table 1). Serum IL-3 could be detected and correlated with the clinical course. When the patient's leukemic cell burden was

highest, the IL-3 level was highest. No serum GM-CSF or IL-5 could be detected.

Since the IL-3 immunoassay measured only immunoreactive factor, we confirmed that biologically active IL-3 was present by using the TF-1 bioassay. This bioassay can be rendered monospecific using appropriate neutralizing monoclonal antibodies specific for IL-3, IL-5, or GM-CSF. We observed that sera from 1-16-84 and 3-14-84 contained TF-1 stimulating activity that could be blocked with anti-IL-3 MoAb (BVD3-6G8), but not with MoAbs to IL-5 (JES1-39D10) or GM-CSF (BVD2-23B6) (Fig 4; GM-CSF data not shown). The amount of neutralizable bioactivity in these two samples correlated very well with the difference in IL-3 levels obtained by immunoassay for these samples. Furthermore, the failure to block TF-1 proliferating activity with either anti-IL-5 or anti-GM-CSF was consistent with the inability to measure these factors by immunoassay and

Table 1. Peripheral Blood Counts and Growth Factor Levels at Different Times in Case 2

	Sample Date		
	11/16/83	1/16/84	3/14/84
Peripheral blood counts (cells/ μ L)			
WBC	81,800	116,500	12,300
Lymphoblasts	0	33,785	0
Eosinophils	46,626	73,080	615
Serum growth factor levels (pg/mL)			
IL-3	<444	7,995	1,051
GM-CSF	<15	<15	<15
IL-5	<50	<50	<50

Peripheral blood counts from Case 2 at three different time points with the corresponding growth factor levels quantified by immunoassay. The patient received chemotherapy between 1/16/84 and 3/14/84 to lower his leukemic burden.³ No serum samples were available for a similar analysis of Case 1.

Abbreviation: WBC, white blood cells.

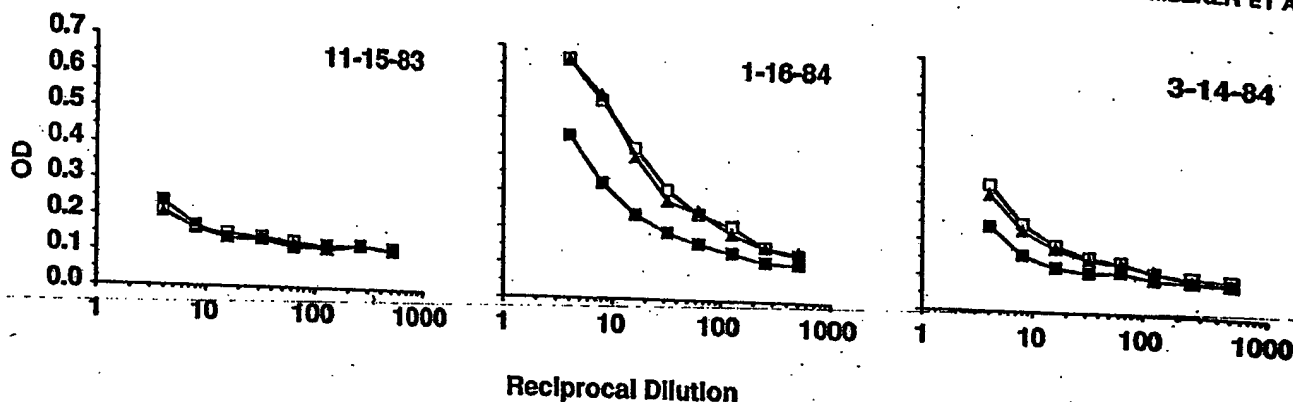


Fig 4. Bloassay of serum IL-3. Leukemia patient sera were tested for bioactive IL-3 and IL-5 in the TF-1 proliferation assay. The reciprocal of the dilution is indicated on the horizontal axis and the optical density indicating the amount of proliferation is indicated on the vertical axis. Serum from all three time points was assayed simultaneously. The assay was rendered monospecific by using a 1 μ g/ml final concentration of monoclonal rat anti-IL-3, BVD3-6G8 (■), or anti-IL-5, JES1-39D10 (□). On 1/16/84 and 3/14/84, inhibition of proliferation was evident in the presence of anti-IL-3 antibody, documenting serum levels of IL-3 on those days. Serum IL-5 was not detected in this assay, as anti-IL-5 did not alter TF-1 proliferation.

indicated that these other myeloid growth factors were not detectably circulating in the serum of this patient.

DISCUSSION

In this report, we have extended our analysis of acute lymphocytic leukemia and eosinophilia associated with the t(5;14) translocation. In both cases we have studied, we have documented the joining of the IL-3 gene from chromosome 5 to the IgH gene from chromosome 14. The breakpoints on chromosome 5 are within 500 bp of each other, suggesting that additional breakpoints will be clustered in a small region of the IL-3 promoter. The PCR assay we have developed will be useful in the screening of additional clinical samples for this abnormality.

The finding of a disrupted IL-3 promoter associated with an otherwise normal IL-3 gene implied that this translocation might lead to the over-expression of a normal IL-3 gene product. In this work, we have documented that this is true. In addition, neither GM-CSF nor IL-5 are over-expressed by the leukemic cells. Furthermore, in one patient, serum IL-3 could be measured and correlated with disease activity. To our knowledge, this is the first measurement of human IL-3 in serum and its association with a disease process. The measurement of serum IL-3 in this and other clinical settings may now be indicated.

The finding of the IL-3 gene adjacent to a cancer-associated translocation breakpoint suggests that its activation is important for oncogenesis. It is our thesis that an autocrine loop for IL-3 is important for the evolution of this leukemia.²¹ The excessive IL-3 production that we have documented would be one feature of such an autocrine loop. The final proof of our thesis must await additional data. In particular, from the study of additional clinical samples, it will be necessary to document that the IL-3 receptor is present on the leukemic cells and that anti-IL-3 antibody decreases proliferation of the leukemia in vitro.

An important aspect of this work is the suggestion of a therapeutic approach for this disease. If an autocrine loop for IL-3 can be documented in this disease, attempts to lower circulating IL-3 levels or block the interaction of IL-3 with its receptor may prove useful. Because it is also possible that the eosinophilia in these patients is mediated by the paracrine effects of leukemia-derived IL-3, similar interventions may improve this aspect of the disease. Antibodies or engineered ligands to accomplish these goals may soon be available.

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Clinical and Pathologic Significance of the *c-erbB-2* (*HER-2/neu*) Oncogene

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The *c-erbB-2* oncogene was first shown to have clinical significance in 1987 by Slamon et al,⁷⁹ who reported that *c-erbB-2* DNA amplification in breast carcinomas correlated with decreased survival in patients with metastasis to axillary lymph nodes. Subsequent studies, however, of *c-erbB-2* activation in breast carcinoma reached conflicting conclusions about its clinical significance. This oncogene also has been reported to have clinical and pathologic implications in other neoplasms. Our review summarizes these various studies and examines the clinical relevance of *c-erbB-2* activation, which has not been emphasized in recent reviews.^{37,38,55} The molecular biology of the *c-erbB-2* oncogene has been extensively reviewed^{37,38,55} and will be discussed only briefly here.

BACKGROUND

The *c-erbB-2* oncogene was discovered in the 1980s by three lines of investigation. The *neu* oncogene was detected as a mutated transforming gene in neuroblastomas induced by ethylnitrosurea treatment of fetal rats.^{8,73,74,75} The *c-erbB-2* was a human gene discovered by its homology to the retroviral gene *v-erbB*.^{33,49,76} *HER-2* was isolated by screening a human genomic DNA library for homology with *v-erbB*.²⁴ When the DNA sequences were determined subsequently, *c-erbB-2*, *HER-2*, and *neu* were found to represent the same gene. Recently, the *c-erbB-2* oncogene also has been referred to as *NGL*.

The *c-erbB-2* DNA is located on human chromosome 17q21^{34,33,55} and codes for *c-erbB-2* mRNA (4.6 kb), which translates *c-erbB-2* protein (p185). This

protein is a normal component of cytoplasmic membranes. The *c-erbB-2* oncogene is homologous with, but not identical to, *c-erbB-1*, which is located on chromosome 7 and codes for the epidermal growth factor receptor.^{4,106} The *c-erbB-2* protein is a receptor on cell membranes and has intracellular tyrosine kinase activity and an extracellular binding domain.^{2,106} Electron microscopy with a polyclonal antibody detects *c-erbB-2* immunoreactivity on cytoplasmic membranes of neoplasms, especially on microvilli and the non-villous outer cell membrane.⁶¹ In normal cells, immunohistochemical reactivity for *c-erbB-2* is frequently present at the basolateral membrane or the cytoplasmic membrane's brush border.^{22,62}

There is experimental evidence that *c-erbB-2* protein may be involved in the pathogenesis of breast neoplasia. Overproduction of otherwise normal *c-erbB-2* protein can transform a cell line into a malignant phenotype.²² Also, when the *neu* oncogene containing an activating point mutation is placed in transgenic mice with a strong promoter for increased expression, the mice develop multiple independent mammary adenocarcinomas.^{12,63} In other experiments, monoclonal antibodies against the *neu* protein inhibit the growth (in nude mice) of a *neu*-transformed cell line,²⁵⁻²⁸ and immunization of mice with *neu* protein protects them from subsequent tumor challenge with the *neu*-transformed cell line.¹⁴ Some authors have speculated that the use of antagonists for the unknown ligand could be useful in future chemotherapy.²⁵ Further review of this experimental evidence is beyond the scope of this article.

The *c-erbB-2* activation most likely occurs at an early stage of neoplastic development. This hypothesis is supported by the presence of *c-erbB-2* activation in both in situ and invasive breast carcinomas. In addition, studies of metastatic breast carcinomas usually demonstrate uniform *c-erbB-2* activation at multiple sites in the same patient,^{11,12,32,41,52} although *c-erbB-2* activation has rarely been detected in metastatic lesions but not in the primary tumor.^{57,66,107} Even more rarely, *c-erbB-2* DNA amplification has been detected in a primary breast carcinoma but not in its lymph node metastasis.⁵ In patients who have bilateral breast neoplasms, both lesions have similar patterns of *c-erbB-2* activation, but only a few such cases have been studied.¹¹

MECHANISMS OF *c-erbB-2* ACTIVATION

The most common mechanism of *c-erbB-2* activation is genomic DNA amplification, which almost always results in overproduction of *c-erbB-2* mRNA and protein.^{17,24,65,81} The *c-erbB-2* amplification may stabilize the overproduction of mRNA or protein through unknown mechanisms. Human breast carcinomas with *c-erbB-2* amplification contain 2 to 40 times more *c-erbB-2* DNA⁴³ and 4 to 128 times more *c-erbB-2* mRNA^{34,60} than found in normal tissue. Most human breast carcinomas with *c-erbB-2* amplification have 2 to 15 times more *c-erbB-2* DNA. Tumors with greater amplification tend to have greater overproduction.^{17,52,65} The non-mammary neoplasms that have been studied tend to have

similar levels of c-erbB-2 amplification or overproduction relative to the corresponding normal tissue.

The second most common mechanism of c-erbB-2 activation is overproduction of c-erbB-2 mRNA and protein without amplification of c-erbB-2 DNA.⁵¹ The quantities of mRNA and protein usually are less than those in amplified cases and may approach the small quantities present in normal breast or other tissues.^{17,52,53} The c-erbB-2 protein overproduction without mRNA overproduction or DNA amplification has been described in a few human breast carcinoma cell lines.⁴⁷

Other rare mechanisms of c-erbB-2 activation have been reported. Translocations involving the c-erbB-2 gene have been described in a few mammary and gastric carcinomas, although some reported cases may represent restriction fragment length polymorphisms or incomplete restriction enzyme digestions that mimic translocations.^{31,53,73,94,100,108} A single point mutation in the transmembrane portion of *neu* has been described in rat neuroblastomas induced by ethylnitrosurea.^{9,55} The mutated *neu* protein has increased tyrosine kinase activity and aggregates at the cell membrane.^{10,53,58} Although there has been speculation that some of the amplified c-erbB-2 genes may contain point mutations,⁴⁸ none has been detected in primary human neoplasms.^{41,53,55}

TECHNIQUES FOR DETECTING c-erbB-2 ACTIVATION

Detection of c-erbB-2 DNA Amplification

Amplification of c-erbB-2 DNA is usually detected by DNA dot blot or Southern blot hybridization. In the dot blot method, the extracted DNA is placed directly on a nylon membrane and hybridized with a c-erbB-2 DNA probe. In the Southern blot method, the extracted DNA is treated with a restriction enzyme, and the fragments are separated by electrophoresis, transferred to a nylon membrane, and hybridized with a c-erbB-2 DNA probe. In both techniques, c-erbB-2 amplification is quantified by comparing the intensity (measured by densitometry) of the hybridization bands from the sample with those from control tissue.

Several technical problems may complicate the measurement of c-erbB-2 DNA amplification. First, the extracted tumor DNA may be excessively degraded or diluted by DNA from stromal cells.⁵¹ Second, the c-erbB-2 DNA probe must be carefully chosen and labeled. For example, oligonucleotide c-erbB-2 probes may not be sensitive enough for measuring a low level of c-erbB-2 amplification, because diploid copy numbers can be difficult to detect (unpublished data). Third, the total amounts of DNA in the sample and control tissue must be compensated for, often with a probe to an unamplified gene. Many studies have used control probes to genes on chromosome 17, the location of c-erbB-2, to correct for possible alterations in chromosome number. Identical results, however, are obtained by using control probes to genes on other chromosomes,^{5,55,80} with rare exception.¹⁷ Studies using control probes to the beta-

globin gene must be interpreted with caution, because one allele of this gene is deleted occasionally in breast carcinomas.²

Amplification of *c-erbB-2* DNA was assessed by using the polymerase chain reaction (PCR) in one recent study.³² Oligoprimers for the *c-erbB-2* gene and a control gene are added to the sample's DNA, and PCR is performed. If the sample contains more copies of *c-erbB-2* DNA than of the control gene, the *c-erbB-2* DNA is replicated preferentially.

Detection of *c-erbB-2* mRNA Overproduction

Overproduction of *c-erbB-2* mRNA usually is measured by RNA dot blot or Northern blot hybridization. Both techniques require extraction of RNA but otherwise are analogous to DNA dot blot and Southern blot hybridization. Use of PCR for detection of *c-erbB-2* mRNA has been described in two recent abstracts.^{33,102}

Overproduction of *c-erbB-2* mRNA can be measured by *in situ* hybridization. Sections are mounted on glass slides, treated with protease, hybridized with a radiolabeled probe, washed, treated with nuclease to remove unbound probe, and developed for autoradiography. Silver grains are seen only over tumor cells that overproduce *c-erbB-2* mRNA. Negative control probes are used.^{33,99,103} Our experience indicates that these techniques are relatively insensitive for detecting *c-erbB-2* mRNA overproduction in routinely processed tissue. Although the sensitivity may be increased by modifications that allow simultaneous detection of *c-erbB-2* DNA and mRNA, *in situ* hybridization still is cumbersome and expensive (unpublished data).

All of the above *c-erbB-2* mRNA detection techniques have several problems that make them more difficult to perform than techniques for detecting DNA amplification. One major problem is the rapid degradation of RNA in tissue that is not immediately frozen or fixed. In addition, during the detection procedure, RNA can be degraded by RNase, a ubiquitous enzyme, which must be eliminated meticulously from laboratory solutions. Third, control probes to genes that are uniformly expressed in the tissue of interest need to be carefully selected.

Detection of *c-erbB-2* Protein Overproduction

The most accurate methods for detecting *c-erbB-2* protein overproduction are the Western blot method and immunoprecipitation. Both techniques can document the binding specificity of various antibodies against *c-erbB-2* protein. In Western blot studies, protein is extracted from the tissue, separated by electrophoresis (according to size), transferred to a membrane, and detected by using antibodies to *c-erbB-2*. In immunoprecipitation studies, antibodies against *c-erbB-2* are added to a tumor lysate, and the resulting protein-antibody precipitate is separated by gel electrophoresis and stained for protein. Both Western blot and immunoprecipitation are useful research tools but currently are not practical for diagnostic pathology. Two recent abstracts have described an enzyme-linked immunosorbent assay (ELISA) for detection of *c-erbB-2* protein.^{12,45}

Overproduction of c-erbB-2 protein is most commonly assessed by various immunohistochemical techniques. These procedures often generate conflicting results, which are explained at least partially by three factors. First, various studies have used different polyclonal and monoclonal antibodies. Because some polyclonal antibodies recognize weak bands in addition to the c-erbB-2 protein band on Western blot or immunoprecipitation, the results of these studies should be interpreted with caution.^{22,24,47,61} Even some monoclonal antibodies immunoprecipitate protein bands in addition to c-erbB-2 (p185).^{20,52,58} Second, tissue fixation contributes to variability between studies. For example, some antibodies detect c-erbB-2 protein only in frozen tissue and do not react in fixed tissue. In general, formalin fixation diminishes the sensitivity of immunohistochemical methods and decreases the number of reactive cells.^{21,28} When Bouin's fixative is used, there may be a higher percentage of positive cases.²² Third, minimal criteria for interpreting immunohistochemical staining are generally lacking. Although there is general agreement that distinct crisp cytoplasmic membrane staining is diagnostic for c-erbB-2 activation in breast carcinoma, the number of positive cells and the staining intensity required to diagnose c-erbB-2 protein overproduction varies from study to study and from antibody to antibody. Degradation of c-erbB-2 protein is not a problem because it can be detected in intact form more than 24 hours after tumor resection without fixation or freezing.⁶⁴

ACTIVATION OF c-erbB-2 IN BREAST LESIONS

Incidence of c-erbB-2 Activation

Most studies of c-erbB-2 oncogene activation do not specify histological subtypes of infiltrating breast carcinoma. Amplification of c-erbB-2 DNA was found in 19.1 percent (519 of 2715) of invasive carcinomas in 25 studies (Table 1), and c-erbB-2 mRNA or protein overproduction was detected in 20.9 percent (566 of 2714) of invasive carcinomas in 20 studies. Twelve studies have documented c-erbB-2 mRNA or protein overproduction in 15 percent (88 of 604) of carcinomas that lacked c-erbB-2 DNA amplification.

The incidence of c-erbB-2 activation in infiltrating breast carcinoma varies with the histological subtype. Approximately 22 percent (142 of 650) of infiltrating ductal carcinomas have c-erbB-2 activation, as expected from the above data. Other variants of breast carcinoma with frequent c-erbB-2 activation are inflammatory carcinoma (62 percent, 54 of 87), Paget's disease (82 percent, 9 of 11), and medullary carcinoma (22 percent, 5 of 23). In contrast, c-erbB-2 activation is infrequent in infiltrating lobular carcinoma (7 percent, 5 of 73) and tubular carcinoma (7 percent, 1 of 15).

The c-erbB-2 protein overproduction is present in 44 percent (44 of 100) of ductal carcinomas in situ and especially comedocarcinoma in situ (68 percent, 49 of 72). The micropapillary type of ductal carcinoma in situ also tends to have c-erbB-2 activation,^{40,54,68} especially if larger cells are present. The greater fre-

TABLE 1. c-erbB-2 ACTIVATION IN MALIGNANT HUMAN BREAST NEOPLASMS

Histological Diagnosis	c-erbB-2 DNA Amplification ^a	c-erbB-2 mRNA Overproduction ^b	c-erbB-2 Protein Overproduction ^c
Carcinoma, not otherwise specified	14/628, ^a 52/310, ¹⁷	42/180, ^a 49/126, ³⁰	118/728, ^{30b}
	52/291, ¹⁰⁰ 28/176, ²⁷	19/62, ³⁰ 19/57, ³⁰	58/330, ^{17b} 47/313, ^{30b}
	17/167, ¹¹³ 22/141, ³⁰	3/11, ³⁰ 6/10, ³⁰ 3/3 ³¹	17/185, ¹¹ 32/191, ³⁰
	14/136, ²⁷ 12/122, ⁴		31/185, ¹⁰¹ 34/102, ³²
	19/103, ⁷⁰ 15/85, ³⁰		24/53, ^{30b} 23/47, ³³
	16/88, ¹¹¹ 17/73, ⁷⁷		22/45, ⁹ 11/36, ³⁴
	16/66, ³² 8/61, ³⁰		7/24, ³¹ 1/10 ³¹
	11/57, ³² 10/57, ³⁰		
	13/51, ¹³ 8/49, ³³		
	10/38, ³² 12/38, ³⁴		
	1/25, ¹⁹ 7/24, ³¹		
	7/15, ³¹ 7/10, ³⁰		
	2/10 ³¹		
	—	18/138, ³¹ 14/73, ³⁴	18/231, ^{17b} 18/136, ³¹
		8/46, ³⁰ 0/8, ³⁰ 1/4, ³¹	13/35, ¹³ 14/28, ^{30b}
		0/3 ³⁰	1/28, ³⁰ 3/24, ³⁴
			0/17 ³¹
Carcinoma, type not specified but lacking c-erbB-2 DNA amplification		35/85 ³⁴	22/137, ³⁰ 14/83, ³⁰
	21/118, ³⁰ 23/107, ³⁴		8/34 ^{30b}
	17/50, ⁴⁴ 7/57 ³⁰		
Infiltrating ductal carcinoma	14/53 (comedo-carcinoma) ¹⁶		
	3/33 (tubuloductal carcinoma) ¹⁶		

Inflammatory carcinoma	33/80, ³⁵ 3/6 ³²	46/75 ³⁸	5/6 ^{32b}
Page's disease	—	—	5/6, ³² 2/3, ³⁴ 2/2 ³⁵
Tubular carcinoma	0/5, ¹⁸ 0/1 ³²	—	1/6 ⁴⁰
Medullary carcinoma	2/4, ¹⁸ 0/1 ³⁴	0/1 ³⁴	1/12, ⁴⁰ 1/3, ³⁵ 1/2, ³²
Mucinous carcinoma	0/1, ¹⁸ 0/1 ³²	—	0/1 ³⁶
Invasive papillary carcinoma	0/2 ³²	—	1/2 ³⁴
Infiltrating lobular carcinoma	1/16, ¹⁸ 0/5 ³⁴	1/5 ³⁴	2/27, ³² 0/12, ⁴⁰ 0/9, ³⁵
Mammary fibrosarcoma	0/1 ³²	—	1/5 ³⁴
"Benign cystosarcoma"	—	1/1 ³²	—
Ductal CIS ^a with minimal invasion	3/5 ³²	—	—
Ductal CIS	0/2 ³⁴	1/2 ³⁴	33/74, ⁴⁰ 10/24 ³⁹
Ductal CIS, solid or comedo type	—	—	20/33, ³⁸ 19/29, ³²
Ductal CIS, micropapillary type	—	—	10/10 ³⁴
Ductal CIS, micropapillary or cribriform type	—	—	10/10 ³⁵
Ductal CIS, papillary or cribriform type	—	—	1/(focal)/14 ³⁴
Lobular CIS	—	—	0/16, ³² 1/8, ³⁵ 0/9 ⁴⁰
	—	—	0/16 ⁴⁰

^aShown as number of cases with activation/number of cases studied; reference is given as a superscript.

^bThese protein studies used Western blot; the rest used immunohistochemical methods.

^cCIS = carcinoma in situ.

quency of *c-erbB-2* protein overproduction in comedocarcinoma in situ, compared with infiltrating ductal carcinoma, could be explained by the fact that many infiltrating ductal carcinomas arise from other types of intraductal carcinoma, which show *c-erbB-2* activation infrequently. Others have speculated that carcinoma in situ with *c-erbB-2* activation tends to regress or to lose *c-erbB-2* activation during progression to invasion.^{41,42,43} Infiltrating and in situ components of ductal carcinoma, however, usually are similar with respect to *c-erbB-2* activation,^{11,39} although some authors have noted more heterogeneity of the immunohistochemical staining pattern in invasive than in in situ carcinoma.^{40,41,43} Activation of *c-erbB-2* is infrequent in lobular carcinoma in situ. If lesions contain more than one histological pattern of carcinoma in situ, the *c-erbB-2* protein overproduction tends to occur in the comedocarcinoma in situ but may include other areas of carcinoma in situ.^{42,44,45} Overproduction of *c-erbB-2* protein in ductal carcinoma in situ correlates with larger cell size and a periductal lymphoid infiltrate.⁴⁶

Activation of *c-erbB-2* has not been identified in benign breast lesions, including fibrocystic disease, fibroadenomas, and radial scars (Table 2). Strong membrane immunohistochemical reactivity for *c-erbB-2* has not been described in atypical ductal hyperplasia, although weak accentuation of membrane staining has been noted infrequently.^{32,42,54} In normal breast tissue, *c-erbB-2* DNA is diploid, and *c-erbB-2* is expressed at lower levels than in activated tumors.^{34,35,55}

These preliminary data suggest that *c-erbB-2* activation may not be useful for resolving many of the common problems in diagnostic surgical pathology. For example, *c-erbB-2* activation is infrequent in tubular carcinoma and radial scars. In addition, because *c-erbB-2* activation is unusual in atypical ductal hyperplasia, cribriform carcinoma in situ, and papillary carcinoma in situ, detection of *c-erbB-2* activation in these lesions may not be helpful in their differential diagnosis. The histological features of comedocarcinoma in situ, which commonly overproduces *c-erbB-2*, are unlikely to be mistaken for those of benign lesions. Activation of

TABLE 2. *c-erbB-2* ACTIVATION IN BENIGN HUMAN BREAST LESIONS

Histological Diagnosis	<i>c-erbB-2</i> DNA Amplification ^a	<i>c-erbB-2</i> mRNA Overproduction	<i>c-erbB-2</i> Protein Overproduction
Fibrocystic disease	0/10 ⁵³	—	0/32, ³⁹ 0/9, ⁵⁵ 0/8 ⁵⁵
Atypical ductal hyperplasia	—	—	2(weak)/21, ⁵⁴ 1(cytoplasmic)/13 ³⁹
Benign ductal hyperplasia	—	—	0/12 ³⁹
Sclerosing adenosis	—	—	0/4 ³⁹
Fibroadenomas	0/16, ³⁴ 0/6, ⁵⁵ 0/2, ²¹ 0/1 ⁵¹	0/6, ³⁵ 0/3 ³⁴	0/21, ³⁹ 0/10, ⁵⁵ 0/8, ⁵⁵ 0/3 ⁴²
Radial scars	—	—	0/22 ³⁹
Blunt duct adenosis	—	—	0/14 ³⁹
"Breast mastoids"	—	0/3 ³⁵	—

^aShown as number of cases with activation/number of cases studied; reference is given as a superscript.

c-erbB-2, however, does favor infiltrating ductal carcinoma over infiltrating lobular carcinoma. Further studies of these issues would be useful.

Correlation of c-erbB-2 Activation With Pathologic Prognostic Factors

Multiple studies have attempted to correlate c-erbB-2 activation with various pathologic prognostic factors (Table 3). Activation of c-erbB-2 was correlated with lymph node metastasis in 8 of 28 series, with higher histological grade in 6 of 17 series, and with higher stage in 4 of 14 series. Large tumor size was not associated with c-erbB-2 activation in most studies (11 of 14). Tetraploid DNA content and low proliferation, measured by Ki-67, have been suggested as prognostic factors and may correlate with c-erbB-2 activation.^{4,7}

Correlation of c-erbB-2 Activation With Clinical Prognostic Factors

Various studies have attempted also to correlate c-erbB-2 activation with clinical features that may predict a poor outcome (Table 4). Activation of c-erbB-2 correlated with absence of estrogen receptors in 10 of 28 series and with absence of progesterone receptors in 6 of 18 series. In most studies, patient age did not correlate with c-erbB-2 activation, and, in the rest of the reports, c-erbB-2 activation was associated with either younger or older ages.

Correlation of c-erbB-2 Activation With Patient Outcome

Slamon et al^{79,81} first showed that amplification of the c-erbB-2 oncogene independently predicts decreased survival of patients with breast carcinoma. The correlation of c-erbB-2 amplification with poor outcome was nearly as strong as the correlation of number of involved lymph nodes with poor outcome. Slamon et al also reported that c-erbB-2 amplification is an important prognostic indicator only in patients with lymph node metastasis.^{79,81}

A large number of subsequent studies also attempted to correlate c-erbB-2 activation with prognosis (Table 5). In 12 series, there was a correlation between c-erbB-2 activation and tumor recurrence or decreased survival. In five of these series, the predictive value of c-erbB-2 activation was reported to be independent of other prognostic factors. In contrast, 18 series did not confirm the correlation of c-erbB-2 activation with recurrence or survival. Four possible explanations for this controversy are discussed below.

One problem is that c-erbB-2 amplification correlates with prognosis mainly in patients with lymph node metastasis. As summarized in Table 5, most studies of patients with axillary lymph node metastasis showed a correlation of c-erbB-2 activation with poor outcome. In contrast, most studies of patients without axillary metastasis have not demonstrated a correlation with patient outcome. Table 6 summarizes the studies in which all patients (with and without axillary metastasis) were considered as one group. There is a trend for studies with a higher percentage of metastatic cases to show an association between c-erbB-2 activation and poor outcome. Thus, most of the current evidence suggests that c-erbB-2 activation has prognostic value only in patients with metastasis to lymph nodes.

*A correlation is statistically significant at <0.05 , equivalent at best between 0.05 and 0.15, and not statistically significant at >0.15 . Numbers inside parentheses are the number of patients in an individual study; superscript is the reference. Some studies analyzed more than one group of patients. By Western blot method; all other protein studies used immunohistochemical methods.

TABLE 4. CORRELATION OF c-erbB-2 ACTIVATION WITH CLINICAL PROGNOSTIC FACTORS IN BREAST CARCINOMA

Prognostic Factor	P ^a	c-erbB-2 DNA Amplification ^b	c-erbB-2 mRNA Overproduction	c-erbB-2 Protein Overproduction ^c
Absence of estrogen receptors	<0.05 0.05-0.15 >0.15	(253) ¹⁰² (141) ⁷⁸ (109) ³⁴ (86) ⁷⁸ (50) ⁴⁴ (47) ¹³ — (157) ¹¹³ (122) ⁴ (103) ⁷⁸ (95) ⁹⁰ (64) ⁷⁷ (61) ⁹⁰ (58) ¹¹¹ (53) ²¹ (51) ³² (41) ³² (253) ¹⁰² (141) ⁷⁸ (109) ³⁴ (86) ⁷⁸ (49) ³² (157) ¹¹³ (122) ⁴ (103) ⁷⁸ (64) ⁷⁷	(104) ³² — (180) ⁹⁰ (62) ³² (82) ³² (57) ³² — (180) ⁹⁰ (103) ³² (82) ³² (58) ³² — — (82) ³²	(350) ³² (330) ¹⁷⁰ (185) ¹⁰¹ — (230) ³² (172) ¹¹ (51) ³² (38) ³² — (350) ³² (306) ¹⁷⁰ — (90) ¹¹ (49) ³² (younger: 330) ¹⁷⁰ (older: 58) ³² — (350) ³² (290) ³² (189) ³² (182) ¹¹ (45) ³²
Absence of progesterone receptors	<0.05 0.05-0.15 >0.15	(253) ¹⁰² (141) ⁷⁸ (109) ³⁴ (86) ⁷⁸ (49) ³² (157) ¹¹³ (122) ⁴ (103) ⁷⁸ (64) ⁷⁷	(104) ³² — (180) ⁹⁰ (103) ³² (82) ³² (58) ³²	(350) ³² (330) ¹⁷⁰ — (90) ¹¹ (49) ³² (younger: 330) ¹⁷⁰ (older: 58) ³² — (350) ³² (290) ³² (189) ³² (182) ¹¹ (45) ³²
Age (menopausal status)	<0.05 0.05-0.15 >0.15	(253) ¹⁰² (141) ⁷⁸ (109) ³⁴ (86) ⁷⁸ (49) ³² (157) ¹¹³ (122) ⁴ (103) ⁷⁸ (64) ⁷⁷	(104) ³² — (180) ⁹⁰ (103) ³² (82) ³² (58) ³²	(350) ³² (330) ¹⁷⁰ — (90) ¹¹ (49) ³² (younger: 330) ¹⁷⁰ (older: 58) ³² — (350) ³² (290) ³² (189) ³² (182) ¹¹ (45) ³²

^aA correlation is statistically significant at <0.05, equivocal at best between 0.05 and 0.15, and not statistically significant at >0.15.
^bNumbers inside parentheses are the number of patients in an individual study; superscript is the reference. Some studies analyzed more than one group of patients.
^cby Western blot method; all other protein studies used immunohistochemical methods.

TABLE 5. CORRELATION OF c-erbB-2 ACTIVATION WITH OUTCOME IN PATIENTS WITH BREAST CARCINOMA

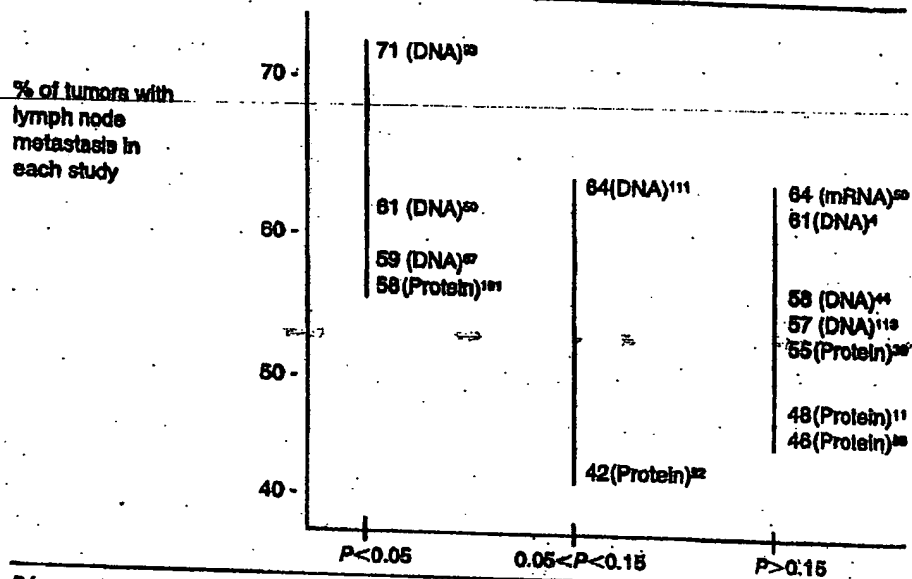
P ^a	Type of c-erbB-2 Activation ^b	Number of Patients		Statistical Analysis ^c	Reference
		Total	With Metastasis to Axillary Lymph Nodes		
<0.05	DNA	176		M	87
<0.05	DNA	61		U	50
<0.05	DNA	57		U	65
<0.05	DNA	41		U	93
<0.05	mRNA	62		U	65
<0.05	Protein	102		M	101
<0.05	DNA		345	M	81
<0.05	DNA		120	U	17
<0.05	DNA		91	U	87
<0.05	DNA		88	M	79
<0.05	Protein-WB		350	M	85
<0.05	Protein		62	U	101
0.05-0.15	DNA	57		U	111
0.05-0.15	Protein	189		M	92
0.05-0.15	Protein		120	U	86
>0.15	DNA	130		U	113
>0.15	DNA	122		M	4
>0.15	DNA	50		U	44
>0.15	mRNA	57		U	50
>0.15	Protein	290		M	86
>0.15	Protein	185		U	11
>0.15	Protein	102		U	39
>0.15	Protein		137	U	17
>0.15	DNA			M	81
>0.15	DNA			U	17
>0.15	DNA			U	87
>0.15	Protein-WB			U	85
>0.15	Protein-WB			U	17
>0.15	Protein			U	86
>0.15	Protein			U	40

^aThe endpoints of these studies were tumor recurrence or decreased survival or both. Correlation between c-erbB-2 activation and a poorer patient outcome is statistically significant at <0.05, is of equivocal significance at 0.05 to 0.15, and is not significant at >0.15.

^bShown as variable measured. Letters "WB" indicate assay by Western blot; the other protein studies used immunohistochemical methods.

^cM = multivariate statistical analysis; U = univariate statistical analysis.

TABLE 6. PERCENTAGE OF BREAST CARCINOMAS WITH METASTASIS COMPARED WITH PROGNOSTIC SIGNIFICANCE OF c-erbB-2 ACTIVATION



P for correlation of c-erbB-2 activation with patient outcome.

Each study's percentage of breast carcinomas with metastasis is compared with the correlation between c-erbB-2 activation and outcome. These data include only those studies that considered, as one group, all breast cancer patients, whether or not they had axillary metastasis. Superscripts are the references. In parentheses are the types of c-erbB-2 activation. P values are interpreted as in Table 3.

A second problem is that various types of breast carcinoma are grouped together in many survival studies. Because the current literature suggests that c-erbB-2 activation is infrequent in lobular carcinoma, studies that combine infiltrating ductal and lobular carcinomas may dilute the prognostic effect of c-erbB-2 activation in ductal tumors. In addition, most studies do not analyze inflammatory breast carcinoma separately. This condition frequently shows c-erbB-2 activation and has a worse prognosis than the usual mammary carcinoma, but it is an uncommon lesion.

A third potential problem is the paucity of studies that attempt to correlate c-erbB-2 activation with clinical outcome in subsets of breast carcinoma without metastasis. Two recent abstracts reported that in patients without lymph node metastasis who had various risk factors for recurrence (such as large tumor size and absence of estrogen receptors), c-erbB-2 overexpression predicted early recurrence.^{23,27} In patients with ductal carcinoma in situ, one small study found no association between tumor recurrence and c-erbB-2 activation.⁴⁰

A fourth problem is the lack of data regarding whether the prognosis correlates better with c-erbB-2 DNA amplification or with mRNA or protein overproduction. Most studies that find a correlation between c-erbB-2 activa-

tion and poor patient outcome measure *c-erbB-2* DNA amplification (Table 5), and breast carcinoma patients with greater amplification of *c-erbB-2* may have poorer survival.^{78,81} Recent studies suggest that amplification has more prognostic power than overproduction,^{17,34,35} but the clinical significance of *c-erbB-2* overproduction without DNA amplification deserves further research.^{17,82} Few studies have attempted to correlate patient outcome with *c-erbB-2* mRNA overproduction, and many studies of *c-erbB-2* protein overproduction use relatively less reliable methods such as immunohistochemical studies with polyclonal antibodies.

Comparison of *c-erbB-2* Activation With Other Oncogenes in Breast Carcinoma

Other oncogenes that may have prognostic implications in human breast cancer are reviewed elsewhere.^{74,108} This section will be restricted to a comparison between the clinical relevance of *c-erbB-2* and these other oncogenes.

The *c-myc* gene is often activated in breast carcinomas, but *c-myc* activation generally has less prognostic importance than *c-erbB-2* activation.^{21,34,77,87,93} One study found a correlation between increased mRNAs of *c-erbB-2* and *c-myc*, although other reports have not confirmed this.^{34,108} Subsequent research, however, could demonstrate a subset of breast carcinomas in which *c-myc* has more prognostic importance than *c-erbB-2*.

The gene *c-erbB-1* for the epidermal growth factor receptor (EGFR) is homologous with *c-erbB-2* but is infrequently amplified in breast carcinomas.⁷⁹ Overproduction of EGFR, however, occurs more frequently than amplification and may correlate with a poor prognosis. In studies that have examined both *c-erbB-2* and EGFR in the same tumor, *c-erbB-2* has a stronger correlation with poor prognostic factors.^{33,82} Studies have tended to show no correlation between amplification of *c-erbB-2* and *c-erbB-1* or overproduction of *c-erbB-2* and EGFR, although at the molecular level EGFR mediates phosphorylation of *c-erbB-2* protein.^{51,82,83,88,109} Recent reviews describe EGFR in breast carcinoma.^{43,100}

The genes *c-erbA* and *ear-1* are homologous to the thyroid hormone receptor, and they are located adjacent to *c-erbB-2* on chromosome 17. These genes are frequently coamplified with *c-erbB-2* in breast carcinomas. The absence of *c-erbA* expression in breast carcinomas, however, is evidence against an important role for this gene in breast neoplasia.⁹⁰ Amplification of *c-erbB-2* can occur without *ear-1* amplification, and these tumors have a decreased survival that is similar to tumors with both *c-erbB-2* and *ear-1* amplification.⁸⁷ Consequently, *c-erbB-2* amplification seems to be more important than amplification of *c-erbA* or *ear-1*.

Other genes also have been compared with *c-erbB-2* activation in breast carcinomas. One study found a significant correlation between increased *c-erbB-2* mRNA and increased mRNAs of *fos*, platelet-derived growth factor chain A, and *Ki-ras*.¹⁰⁸ Allelic deletion of *c-Ha-ras* may indicate a poorer prognosis in breast carcinoma,²¹ but it has not been compared with *c-erbB-2* activation. Some studies have suggested a correlation between advanced stage or recurrence of breast carcinoma and activation of any one of several oncogenes.^{21,113}

ACTIVATION OF c-erbB-2 IN NON-MAMMARY TISSUES

Incidence of c-erbB-2 Activation in Non-Mammary Tissues

Table 7 summarizes the normal tissues in which c-erbB-2 expression has been detected, usually with immunohistochemical methods using polyclonal anti-

TABLE 7. PRESENCE OR ABSENCE OF c-erbB-2 mRNA OR c-erbB-2 PROTEIN IN NORMAL HUMAN TISSUES

Tissues With c-erbB-2 mRNA	Tissues Producing c-erbB-2 Protein ^a	Tissues Lacking c-erbB-2 mRNA	Tissues Lacking c-erbB-2 Protein
Skin ²⁴	Epidermis ²² External root sheath ²² Eccrine sweat gland ²² Fetal oral mucosa ²² Fetal esophagus ²²		Postnatal oral mucosa ²² Postnatal esophagus ²²
Stomach ²⁴	Stomach ^{22,23} Fetal intestine ^{22,23}		
Jejunum ²⁴	Small intestine ^{22,23}		
Colon ²⁴	Colon ^{22,23}		
Kidney ²⁴	Fetal kidney ^{22,23} Fetal proximal tubule ²² Distal tubule ²² Fetal collecting duct ²² Fetal renal pelvis ²² Fetal ureter ²²	Kidneys ¹⁰⁴	Glomerulus ²² Postnatal Bowman's capsule ²² Postnatal proximal tubule ²² Postnatal collecting duct ²² Postnatal renal pelvis ²² Postnatal fetal ureter ²²
Liver ²⁴	Hepatocytes ²² Pancreatic acini ²² Pancreatic ducts ^{22,23} Endocrine cells of islets of Langerhans ²²		Liver ^{22,23} Pancreatic islets ²²
Lung ²⁴	Fetal trachea ²² Fetal bronchioles ²² Bronchioles ²²		Postnatal trachea ²² Postnatal bronchioles ²² Postnatal alveoli ^{22,23}
Fetal brain ²⁴	Fetal ganglion cells ²²		Postnatal brain ²² Postnatal ganglion cells ²²
Thyroid ¹			
Uterus ²⁴	Ovary ¹² Blood vessels ⁴²		Endothelium ²²
Placenta ²⁴			Adrenocortical cells ²² Postnatal thymus ²² Fibroblasts ²² Smooth muscle cells ²² Cardiac muscle cells ²²

^aThis protein study used Western blots; the rest used immunohistochemical methods.

bodies. Only a few studies have been performed, and some of these do not demonstrate convincing cell membrane reactivity in the published photographs. The interpretations in these studies, however, are listed, with the caveat that these findings should be confirmed by immunoprecipitation or Western or RNA blots. Production of *c-erbB-2* has been identified in normal epithelium of the gastrointestinal tract and skin. Discrepancies regarding *c-erbB-2* protein in other tissues could be due, at least in part, to differences in techniques.

The data on *c-erbB-2* activation in various non-mammary neoplasms should be interpreted with caution, because only small numbers of tumors have been studied, usually by immunohistochemical methods using polyclonal antibodies. Studies using cell lines have been excluded, because cell culture can induce amplification and overexpression of other genes, although this has not been documented for *c-erbB-2*.

Activation of *c-erbB-2* has been identified in 32 percent (64 of 203) of ovarian carcinomas in eight studies (Table 8). One abstract⁴⁵ stated that ovarian carcinomas contained significantly more *c-erbB-2* protein than ovarian non-epithelial malignancies. Another report⁴¹ showed that 12 percent of ovarian carcinomas had *c-erbB-2* overproduction without amplification.

Activation of *c-erbB-2* has been identified in 20 percent (40 of 198) of gastric adenocarcinomas in seven studies, including 33 percent (21 of 64) of

TABLE 8. *c-erbB-2* ACTIVATION IN HUMAN GYNECOLOGIC TUMORS*

Tumor Type	<i>c-erbB-2</i> DNA Amplification	<i>c-erbB-2</i> mRNA Over-production	<i>c-erbB-2</i> Protein Over-production
Ovary—carcinoma, not otherwise specified	31/120, ⁶¹ 1/11, ⁵⁷ 0/5, ¹⁰⁷ 0/5, ⁶⁴ 0/3, ¹¹⁸ 0/2, ⁷² 0/1 ¹¹⁰	23/67 ⁶¹	23/73, ¹² 36/72 ⁶¹
Ovary—serous (papillary) carcinoma	2/7, ¹¹⁰ 1/7, ¹¹² 0/6 ⁷²	—	—
Ovary—endometrioid carcinoma	0/3 ¹¹⁰	—	—
Ovary—mucinous carcinoma	1/2, ¹¹⁰ 0/1 ⁷²	—	—
Ovary—clear cell carcinoma	0/2, ¹¹² 0/1 ⁷²	—	—
Ovary—mixed epithelial carcinoma	0/2 ⁷²	—	—
Ovary—endometrioid borderline tumor	0/1 ⁷²	—	—
Ovary—mucinous borderline tumor	0/3 ⁷²	—	—
Ovary—serous cystadenoma	0/4 ⁷²	—	—
Ovary—mucinous cystadenoma	0/2 ⁷²	—	—
Ovary—sclerosing stromal tumor	0/1 ⁷²	—	—
Ovary—fibrothecoma	0/1 ⁷²	—	—
Uterus—endometrial adenocarcinoma	0/4, ⁶⁴ 0/1 ¹¹⁰	—	—

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods.

intestinal or tubular subtypes and 9 percent (4 of 47) of diffuse or signet ring cell subtypes (Table 9). Activation of c-erbB-2 has been detected in 2 percent (6 of 281) of colorectal carcinomas, although an additional immunohistochemical study detected c-erbB-2 protein in seven of eight tissues fixed in Bouin's solution. One study found greater immunohistochemical reactivity for c-erbB-2 protein in colonic adenomatous polyps than in the adjacent normal epithelium, using Bouin's fixative. Lesions with anaplastic features and progression to invasive carcinoma tended to show decreased immunohistochemical reactivity for c-erbB-2 protein.²³ Hepatocellular carcinomas (12 of 14 cases) and cholangiocarcinomas (46 of 63 cases) reacted with antibodies against c-erbB-2 in one study, but some of these "positive" cases showed only diffuse cytoplasmic staining, which

TABLE 9. c-erbB-2 ACTIVATION IN HUMAN GASTROINTESTINAL TUMORS*

Tumor Type	c-erbB-2 DNA Amplification	c-erbB-2 Protein Overproduction
Esophagus—squamous cell carcinoma	0/1 ¹⁰⁷	0/1 ⁸¹
Stomach—carcinoma, poorly differentiated	0/22 ¹⁰⁸	—
Stomach—adenocarcinoma	2/24, ⁸⁴ 2/9, ¹⁰⁷ 2/8, ¹¹¹ 2/8, ⁸⁷ 0/1 ¹⁰⁸	4/27, ²⁸ 3/10 ⁸¹
Stomach—carcinoma, intestinal or tubular type	5/10 ¹⁰⁸	16/54 ²⁸
Stomach—carcinoma, diffuse or signet ring cell type	0/2 ¹⁰⁸	4/45 ²⁸
Colorectum—carcinoma	2/49, ⁸⁴ 1/45, ¹¹¹ 1/45, ⁸⁷ 1/45, ⁸⁰ 0/40, ⁸¹ 0/32, ¹⁰⁷ 0/3 ⁸²	1/22, ⁵⁸ 7/8 ²²⁸
Colon—villous adenoma	0/1 ⁸⁰	—
Colon—tubulovillous adenoma	0/5 ⁸⁰	—
Colon—tubular adenoma	0/7 ⁸⁰	19/19 ²²⁸
Colon—hyperplastic polyp	0/1 ⁸⁰	—
Intestine—leiomyosarcoma	—	0/1 ⁸¹
Hepatocellular carcinoma	0/12 ¹¹¹	12/14, ³⁸ 0/2 ⁸¹
Hepatoblastoma	0/1 ⁸⁷	—
Cholangiocarcinoma	—	46/63 ⁸⁸
Pancreas—adenocarcinoma	—	2/80, ^{41c} 0/2 ⁸¹
Pancreas—acinar carcinoma	—	0/1 ⁸¹
Pancreas—clear cell carcinoma	—	0/2 ⁸¹
Pancreas—large cell carcinoma	—	0/3 ⁸¹
Pancreas—signet ring carcinoma	—	0/1 ⁸¹
Pancreas—chronic inflammation	—	0/14 ^{41c}

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods. No studies analyzed for c-erbB-2 mRNA.

^bTissues fixed in Bouin's solution.

^cOnly cases with distinct membrane staining are interpreted as showing c-erbB-2 overproduction.

TABLE 10. *c-erbB-2* ACTIVATION IN HUMAN PULMONARY TUMORS^a

Tumor Type	<i>c-erbB-2</i> DNA Amplification	<i>c-erbB-2</i> Protein Overproduction
Non-small cell carcinoma	2/60, ⁷⁸ 0/60 ⁸¹	1/84 ⁸²
Epidermoid carcinoma	0/13, ⁸³ 0/10, ⁸⁷ 0/6 ⁸⁸	3/5 ⁸⁸
Adenocarcinoma	0/21, ⁸⁸ 1/13, ⁸⁹ 0/7, ¹¹¹ 0/7, ⁸⁷ 0/3 ¹⁰⁷	4/12 ⁸⁸
Large cell carcinoma	0/9, ⁸⁸ 0/6 ⁸⁹	—
Small cell carcinoma	—	0/26, ⁸⁸ 0/3 ⁸⁹
Carcinoid tumor	0/1 ⁸⁸	0/3 ⁸⁸

^aShown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods. No studies analyzed for *c-erbB-2* mRNA.

does not indicate *c-erbB-2* activation in breast neoplasms.⁸⁵ Also, some pancreatic carcinomas and chronic pancreatitis tissue had cytoplasmic immunohistochemical reactivity for *c-erbB-2* protein, in addition to the rare case of pancreatic adenocarcinoma with distinct cell membrane staining.⁴¹

Tables 10 through 14 summarize the studies of *c-erbB-2* activation in other neoplasms. The *c-erbB-2* oncogene is not activated in most of these tumors. Activation of *c-erbB-2* has been detected in 1 percent (4 of 299) of pulmonary non-small cell carcinomas in nine studies, although one additional report⁸⁹ found *c-erbB-2* protein overproduction in 41 percent (7 of 17). Renal cell carcinoma had *c-erbB-2* activation in 7 percent (2 of 30) in four studies. Overproduction of *c-erbB-2* protein was described in one transitional cell carcinoma of the urinary bladder, a grade 2 papillary lesion.⁸⁸ Squamous cell carcinoma and basal cell carcinoma of the skin may contain *c-erbB-2* protein, but it is not clear

TABLE 11. *c-erbB-2* ACTIVATION IN HUMAN HEMATOLOGIC PROLIFERATIONS^a

Tumor Type	<i>c-erbB-2</i> DNA Amplification	<i>c-erbB-2</i> mRNA Overproduction	<i>c-erbB-2</i> Protein Overproduction
Hematologic malignancies	0/23 ¹¹¹	—	—
Malignant lymphoma	0/9, ⁸⁷ 0/3 ¹⁰⁷	0/1 ¹	0/15 ⁸¹
Acute leukemia	0/14 ⁸⁷	—	—
Acute lymphoblastic leukemia	0/1 ¹⁰⁷	—	—
Acute myeloblastic leukemia	0/3 ¹⁰⁷	—	—
Chronic leukemia	0/19 ⁸⁷	—	—
Chronic lymphocytic leukemia	0/8 ¹⁰⁷	—	—
Chronic myelogenous leukemia	0/8 ¹⁰⁷	—	—
Myeloproliferative disorder	0/1 ⁸⁷	—	—

^aShown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods.

TABLE 12. c-erbB-2 ACTIVATION IN HUMAN TUMORS OF SOFT TISSUE AND BONE*

Tumor Type	c-erbB-2 DNA Amplification
Sarcoma	0/10, ¹¹¹ 0/8 ⁹⁷
Malignant fibrous histiocytoma	0/1 ¹⁰⁷
Liposarcoma	0/3 ¹⁰⁷
Pleomorphic sarcoma	0/1 ¹⁰⁷
Rhabdomyosarcoma	0/1 ¹⁰⁷
Osteogenic sarcoma	0/2, ¹⁰⁷ 0/2 ⁹⁷
Chondrosarcoma	0/1 ¹⁰⁷
Ewing's sarcoma	0/1 ⁹⁷
Schwannoma	0/1 ⁹⁷

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. No studies analyzed for c-erbB-2 mRNA or c-erbB-2 protein.

whether the protein level is increased over that of normal skin.⁵⁸ Thyroid carcinomas and adenomas can have low levels of increased c-erbB-2 mRNA. One abstract described low-level c-erbB-2 DNA amplification in one of ten salivary gland pleomorphic adenomas.⁴²

Correlation of c-erbB-2 Activation With Patient Outcome

Very few studies have attempted to correlate c-erbB-2 activation in non-mammary tumors with outcome. Slamon et al⁹¹ showed that c-erbB-2 amplification or overexpression in ovarian carcinomas correlates with decreased survival, especially when marked activation is present. However, they did not report the stage, histological grade, or histological subtype of these neoplasms. Another study of stages III and IV ovarian carcinomas found a correlation between decreased survival and c-erbB-2 protein overproduction, but not between survival and histological grade.¹² One abstract stated that c-erbB-2 protein overproduction in 10 of 16 pulmonary adenocarcinomas correlated with decreased disease-free interval.⁷⁰ Another abstract described a tendency for immunohisto-

TABLE 13. c-erbB-2 ACTIVATION IN HUMAN TUMORS OF THE URINARY TRACT*

Tumor Type	c-erbB-2 DNA Amplification	c-erbB-2 mRNA Overproduction	c-erbB-2 Protein Overproduction
Kidney—renal cell carcinoma	1/5, ⁹⁷ 1/4, ¹⁰⁷ 0/5 ⁹⁴	0/16 ¹⁰⁴	—
Wilms' tumor	0/4 ⁹⁷	—	—
Prostate—adenocarcinoma	—	—	0/23 ⁹⁸
Urinary bladder—carcinoma	—	—	1/46 ⁹⁸

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods.

TABLE 14. *c-erbB-2* ACTIVATION IN MISCELLANEOUS HUMAN TUMORS^a

Tumor Type	<i>c-erbB-2</i> DNA Amplification	<i>c-erbB-2</i> mRNA Overproduction	<i>c-erbB-2</i> Protein Overproduction
Skin—malignant melanoma	—	—	0/10 ²⁸
Skin, head and neck—squamous cell carcinoma	0/7 ¹⁰⁷	—	—
Site not stated—squamous cell carcinoma	0/3, ⁸⁷ 0/2 ⁷⁸	—	—
Salivary gland—adenocarcinoma	1/1 ⁷⁸	—	—
Parotid gland—adenoid cystic carcinoma	—	—	0/1 ⁸⁸
Thyroid—anaplastic carcinoma	0/1 ¹	0/1 ¹	—
Thyroid—papillary carcinoma	0/5 ¹	3(low levels)/5 ¹	—
Thyroid—adenocarcinoma	0/1 ⁸⁴	—	—
Thyroid—adenoma	0/2 ¹	1(low levels)/2 ¹	—
Neuroblastoma	0/35, ⁸⁹ 0/9, ⁸⁷ 0/1 ⁷⁸	—	—
Meningioma	0/2 ⁸⁷	—	—

^aShown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods.

chemical reactivity for *c-erbB-2* protein to correlate with higher grades of prostatic adenocarcinoma.⁸⁷ Additional prognostic studies of ovarian carcinomas and other neoplasms are needed.

SUMMARY

Activation of the *c-erbB-2* oncogene can occur by amplification of *c-erbB-2* DNA and by overproduction of *c-erbB-2* mRNA and *c-erbB-2* protein. Approximately 20 percent of breast carcinomas show evidence of *c-erbB-2* activation, which correlates with a poor prognosis primarily in patients with metastasis to axillary lymph nodes. Studies that have attempted to correlate *c-erbB-2* activation with other prognostic factors in breast carcinoma have reported conflicting conclusions. The pathologic and clinical significance of *c-erbB-2* activation in other neoplasms is unclear and should be assessed by additional studies.

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DECLARATION OF PAUL POLAKIS, Ph.D.

I, Paul Polakis, Ph.D., declare and say as follows:

1. I was awarded a Ph.D. by the Department of Biochemistry of the Michigan State University in 1984. My scientific Curriculum Vitae is attached to and forms part of this Declaration (Exhibit A).
2. I am currently employed by Genentech, Inc. where my job title is Staff Scientist. Since joining Genentech in 1999, one of my primary responsibilities has been leading Genentech's Tumor Antigen Project, which is a large research project with a primary focus on identifying tumor cell markers that find use as targets for both the diagnosis and treatment of cancer in humans.
3. As part of the Tumor Antigen Project, my laboratory has been analyzing differential expression of various genes in tumor cells relative to normal cells. The purpose of this research is to identify proteins that are abundantly expressed on certain tumor cells and that are either (i) not expressed, or (ii) expressed at lower levels, on corresponding normal cells. We call such differentially expressed proteins "tumor antigen proteins". When such a tumor antigen protein is identified, one can produce an antibody that recognizes and binds to that protein. Such an antibody finds use in the diagnosis of human cancer and may ultimately serve as an effective therapeutic in the treatment of human cancer.
4. In the course of the research conducted by Genentech's Tumor Antigen Project, we have employed a variety of scientific techniques for detecting and studying differential gene expression in human tumor cells relative to normal cells, at genomic DNA, mRNA and protein levels. An important example of one such technique is the well known and widely used technique of microarray analysis which has proven to be extremely useful for the identification of mRNA molecules that are differentially expressed in one tissue or cell type relative to another. In the course of our research using microarray analysis, we have identified approximately 200 gene transcripts that are present in human tumor cells at significantly higher levels than in corresponding normal human cells. To date, we have generated antibodies that bind to about 30 of the tumor antigen proteins expressed from these differentially expressed gene transcripts and have used these antibodies to quantitatively determine the level of production of these tumor antigen proteins in both human cancer cells and corresponding normal cells. We have then compared the levels of mRNA and protein in both the tumor and normal cells analyzed.
5. From the mRNA and protein expression analyses described in paragraph 4 above, we have observed that there is a strong correlation between changes in the level of mRNA present in any particular cell type and the level of protein

expressed from that mRNA in that cell type. In approximately 80% of our observations we have found that increases in the level of a particular mRNA correlates with changes in the level of protein expressed from that mRNA when human tumor cells are compared with their corresponding normal cells.

6. Based upon my own experience accumulated in more than 20 years of research, including the data discussed in paragraphs 4 and 5 above and my knowledge of the relevant scientific literature, it is my considered scientific opinion that for human genes, an increased level of mRNA in a tumor cell relative to a normal cell typically correlates to a similar increase in abundance of the encoded protein in the tumor cell relative to the normal cell. In fact, it remains a central dogma in molecular biology that increased mRNA levels are predictive of corresponding increased levels of the encoded protein. While there have been published reports of genes for which such a correlation does not exist, it is my opinion that such reports are exceptions to the commonly understood general rule that increased mRNA levels are predictive of corresponding increased levels of the encoded protein.

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Dated: 5/07/04

By: Paul Polakis

Paul Polakis, Ph.D.

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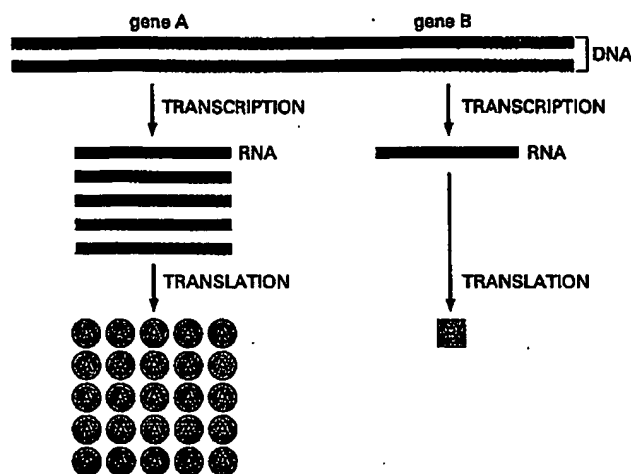


Figure 6-3 Genes can be expressed with different efficiencies. Gene A is transcribed and translated much more efficiently than gene B. This allows the amount of protein A in the cell to be much greater than that of protein B.

FROM DNA TO RNA

Transcription and translation are the means by which cells read out, or express, the genetic instructions in their genes. Because many identical RNA copies can be made from the same gene, and each RNA molecule can direct the synthesis of many identical protein molecules, cells can synthesize a large amount of protein rapidly when necessary. But each gene can also be transcribed and translated with a different efficiency, allowing the cell to make vast quantities of some proteins and tiny quantities of others (Figure 6-3). Moreover, as we see in the next chapter, a cell can change (or regulate) the expression of each of its genes according to the needs of the moment—most obviously by controlling the production of its RNA.

Portions of DNA Sequence Are Transcribed into RNA

The first step a cell takes in reading out a needed part of its genetic instructions is to copy a particular portion of its DNA nucleotide sequence—a gene—into an RNA nucleotide sequence. The information in RNA, although copied into another chemical form, is still written in essentially the same language as it is in DNA—the language of a nucleotide sequence. Hence the name **transcription**.

Like DNA, RNA is a linear polymer made of four different types of nucleotide subunits linked together by phosphodiester bonds (Figure 6-4). It differs from DNA chemically in two respects: (1) the nucleotides in RNA are *ribonucleotides*—that is, they contain the sugar ribose (hence the name *ribonucleic acid*) rather than deoxyribose; (2) although, like DNA, RNA contains the bases adenine (A), guanine (G), and cytosine (C), it contains the base uracil (U) instead of the thymine (T) in DNA. Since U, like T, can base-pair by hydrogen-bonding with A (Figure 6-5), the complementary base-pairing properties described for DNA in Chapters 4 and 5 apply also to RNA (in RNA, G pairs with C, and A pairs with U). It is not uncommon, however, to find other types of base pairs in RNA: for example, G pairing with U occasionally.

Despite these small chemical differences, DNA and RNA differ quite dramatically in overall structure. Whereas DNA always occurs in cells as a double-stranded helix, RNA is single-stranded. RNA chains therefore fold up into a variety of shapes, just as a polypeptide chain folds up to form the final shape of a protein (Figure 6-6). As we see later in this chapter, the ability to fold into complex three-dimensional shapes allows some RNA molecules to have structural and catalytic functions.

Transcription Produces RNA Complementary to One Strand of DNA

All of the RNA in a cell is made by DNA transcription, a process that has certain similarities to the process of DNA replication discussed in Chapter 5.

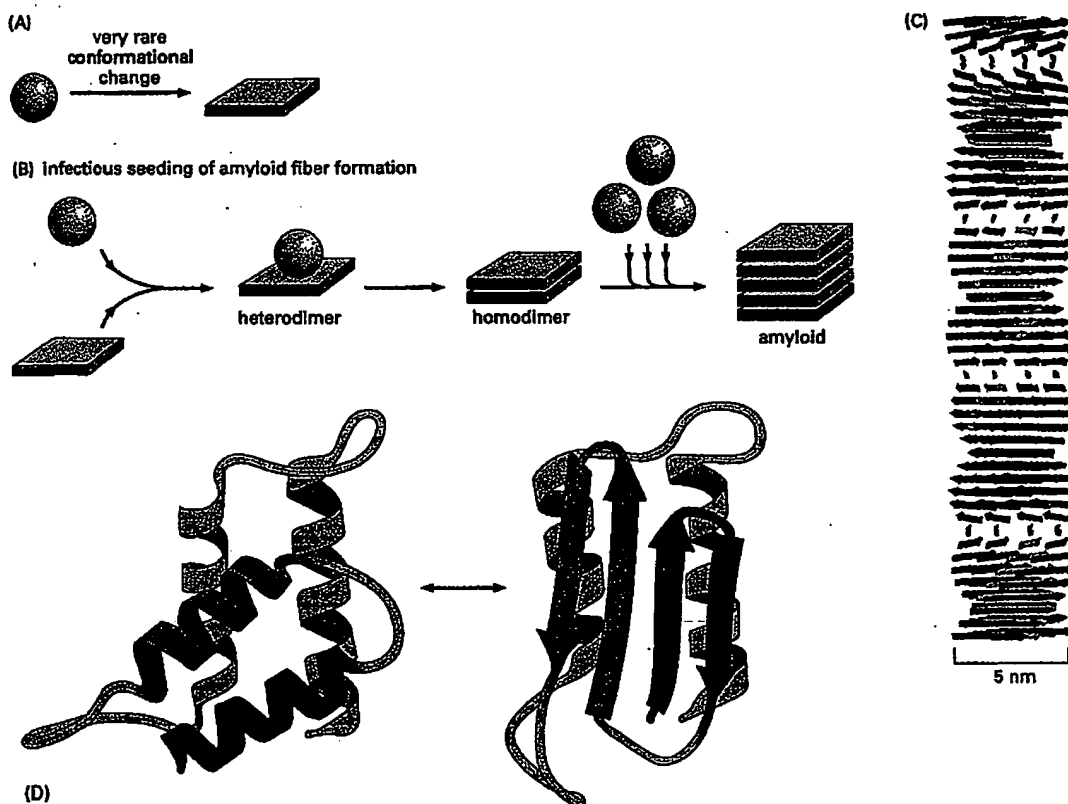


Figure 6-89 Protein aggregates that cause human disease. (A) Schematic illustration of the type of conformational change in a protein that produces material for a cross-beta filament. (B) Diagram illustrating the self-infectious nature of the protein aggregation that is central to prion diseases. PrP is highly unusual because the misfolded version of the protein, called PrP^{*}, induces the normal PrP protein it contacts to change its conformation, as shown. Most of the human diseases caused by protein aggregation are caused by the overproduction of a variant protein that is especially prone to aggregation, but because this structure is not infectious in this way, it cannot spread from one animal to another. (C) Drawing of a cross-beta filament, a common type of protease-resistant protein aggregate found in a variety of human neurological diseases. Because the hydrogen-bond interactions in a β sheet form between polypeptide backbone atoms (see Figure 3-9), a number of different abnormally folded proteins can produce this structure. (D) One of several possible models for the conversion of PrP to PrP^{*}, showing the likely change of two α -helices into four β -strands. Although the structure of the normal protein has been determined accurately, the structure of the infectious form is not yet known with certainty because the aggregation has prevented the use of standard structural techniques. (C, courtesy of Louise Serpell, adapted from M. Sunde et al., *J. Mol. Biol.* 273:729-739, 1997; D, adapted from S.B. Prusiner, *Trends Biochem. Sci.* 21:482-487, 1996.)

animals and humans. It can be dangerous to eat the tissues of animals that contain PrP^{*}, as witnessed most recently by the spread of BSE (commonly referred to as the "mad cow disease") from cattle to humans in Great Britain.

Fortunately, in the absence of PrP^{*}, PrP is extraordinarily difficult to convert to its abnormal form. Although very few proteins have the potential to misfold into an infectious conformation, a similar transformation has been discovered to be the cause of an otherwise mysterious "protein-only inheritance" observed in yeast cells.

There Are Many Steps From DNA to Protein

We have seen so far in this chapter that many different types of chemical reactions are required to produce a properly folded protein from the information contained in a gene (Figure 6-90). The final level of a properly folded protein in a cell therefore depends upon the efficiency with which each of the many steps is performed.

We discuss in Chapter 7 that cells have the ability to change the levels of their proteins according to their needs. In principle, any or all of the steps in Fig-

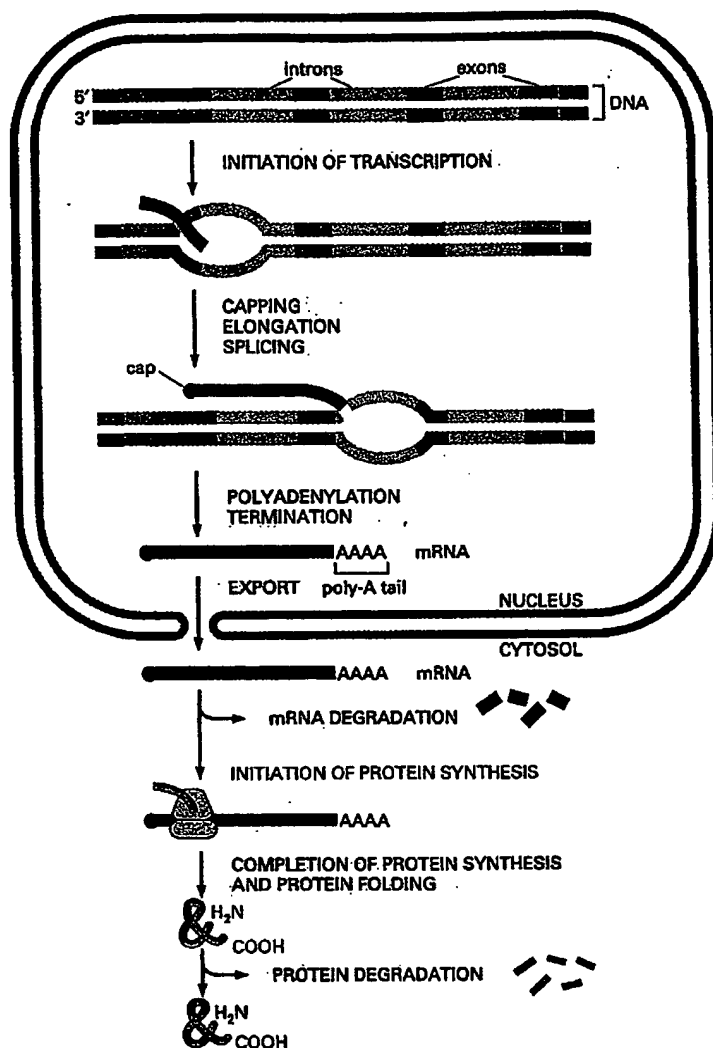


Figure 6-90 The production of a protein by a eucaryotic cell. The final level of each protein in a eucaryotic cell depends upon the efficiency of each step depicted.

ure 6-90) could be regulated by the cell for each individual protein. However, as we shall see in Chapter 7, the initiation of transcription is the most common point for a cell to regulate the expression of each of its genes. This makes sense, inasmuch as the most efficient way to keep a gene from being expressed is to block the very first step—the transcription of its DNA sequence into an RNA molecule.

Summary

The translation of the nucleotide sequence of an mRNA molecule into protein takes place in the cytoplasm on a large ribonucleoprotein assembly called a ribosome. The amino acids used for protein synthesis are first attached to a family of tRNA molecules, each of which recognizes, by complementary base-pair interactions, particular sets of three nucleotides in the mRNA (codons). The sequence of nucleotides in the mRNA is then read from one end to the other in sets of three according to the genetic code.

To initiate translation, a small ribosomal subunit binds to the mRNA molecule at a start codon (AUG) that is recognized by a unique initiator tRNA molecule. A large ribosomal subunit binds to complete the ribosome and begin the elongation phase of protein synthesis. During this phase, aminoacyl tRNAs—each bearing a specific amino acid bind sequentially to the appropriate codon in mRNA by forming complementary base pairs with the tRNA anticodon. Each amino acid is added to the C-terminal end of the growing polypeptide by means of a cycle of three sequential

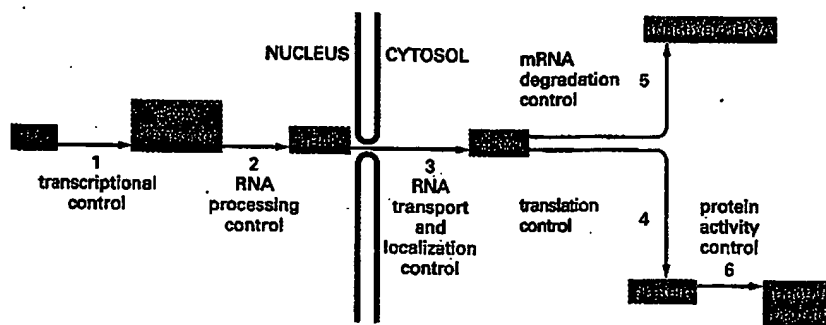


Figure 7-5 Six steps at which eucaryotic gene expression can be controlled. Controls that operate at steps 1 through 5 are discussed in this chapter. Step 6, the regulation of protein activity, includes reversible activation or inactivation by protein phosphorylation (discussed in Chapter 3) as well as irreversible inactivation by proteolytic degradation (discussed in Chapter 6).

Gene Expression Can Be Regulated at Many of the Steps in the Pathway from DNA to RNA to Protein

If differences among the various cell types of an organism depend on the particular genes that the cells express, at what level is the control of gene expression exercised? As we saw in the last chapter, there are many steps in the pathway leading from DNA to protein, and all of them can in principle be regulated. Thus a cell can control the proteins it makes by (1) controlling when and how often a given gene is transcribed (**transcriptional control**), (2) controlling how the RNA transcript is spliced or otherwise processed (**RNA processing control**), (3) selecting which completed mRNAs in the cell nucleus are exported to the cytosol and determining where in the cytosol they are localized (**RNA transport and localization control**), (4) selecting which mRNAs in the cytoplasm are translated by ribosomes (**translational control**), (5) selectively destabilizing certain mRNA molecules in the cytoplasm (**mRNA degradation control**), or (6) selectively activating, inactivating, degrading, or compartmentalizing specific protein molecules after they have been made (**protein activity control**) (Figure 7-5).

For most genes transcriptional controls are paramount. This makes sense because, of all the possible control points illustrated in Figure 7-5, only transcriptional control ensures that the cell will not synthesize superfluous intermediates. In the following sections we discuss the DNA and protein components that perform this function by regulating the initiation of gene transcription. We shall return at the end of the chapter to the additional ways of regulating gene expression.

Summary

The genome of a cell contains in its DNA sequence the information to make many thousands of different protein and RNA molecules. A cell typically expresses only a fraction of its genes, and the different types of cells in multicellular organisms arise because different sets of genes are expressed. Moreover, cells can change the pattern of genes they express in response to changes in their environment, such as signals from other cells. Although all of the steps involved in expressing a gene can in principle be regulated, for most genes the initiation of RNA transcription is the most important point of control.

DNA-BINDING MOTIFS IN GENE REGULATORY PROTEINS

How does a cell determine which of its thousands of genes to transcribe? As mentioned briefly in Chapters 4 and 6, the transcription of each gene is controlled by a regulatory region of DNA relatively near the site where transcription begins. Some regulatory regions are simple and act as switches that are thrown by a single signal. Many others are complex and act as tiny microprocessors, responding to a variety of signals that they interpret and integrate to switch the neighboring gene on or off. Whether complex or simple, these switching devices

occur in the germ line, the cell lineage that gives rise to sperm or eggs. Most of the DNA in vertebrate germ cells is inactive and highly methylated. Over long periods of evolutionary time, the methylated CG sequences in these inactive regions have presumably been lost through spontaneous deamination events that were not properly repaired. However promoters of genes that remain active in the germ cell lineages (including most housekeeping genes) are kept unmethylated, and therefore spontaneous deaminations of Cs that occur within them can be accurately repaired. Such regions are preserved in modern day vertebrate cells as CG islands. In addition, any mutation of a CG sequence in the genome that destroyed the function or regulation of a gene in the adult would be selected against, and some CG islands are simply the result of a higher than normal density of critical CG sequences.

The mammalian genome contains an estimated 20,000 CG islands. Most of the islands mark the 5' ends of transcription units and thus, presumably, of genes. The presence of CG islands often provides a convenient way of identifying genes in the DNA sequences of vertebrate genomes.

Summary

The many types of cells in animals and plants are created largely through mechanisms that cause different genes to be transcribed in different cells. Since many specialized animal cells can maintain their unique character through many cell division cycles and even when grown in culture, the gene regulatory mechanisms involved in creating them must be stable once established and heritable when the cell divides. These features endow the cell with a memory of its developmental history. Bacteria and yeasts provide unusually accessible model systems in which to study gene regulatory mechanisms. One such mechanism involves a competitive interaction between two gene regulatory proteins, each of which inhibits the synthesis of the other; this can create a flip-flop switch that switches a cell between two alternative patterns of gene expression. Direct or indirect positive feedback loops, which enable gene regulatory proteins to perpetuate their own synthesis, provide a general mechanism for cell memory. Negative feedback loops with programmed delays form the basis for cellular clocks.

In eucaryotes the transcription of a gene is generally controlled by combinations of gene regulatory proteins. It is thought that each type of cell in a higher eucaryotic organism contains a specific combination of gene regulatory proteins that ensures the expression of only those genes appropriate to that type of cell. A given gene regulatory protein may be active in a variety of circumstances and typically is involved in the regulation of many genes.

In addition to diffusible gene regulatory proteins, inherited states of chromatin condensation are also used by eucaryotic cells to regulate gene expression. An especially dramatic case is the inactivation of an entire X chromosome in female mammals. In vertebrates DNA methylation also functions in gene regulation, being used mainly as a device to reinforce decisions about gene expression that are made initially by other mechanisms. DNA methylation also underlies the phenomenon of genomic imprinting in mammals, in which the expression of a gene depends on whether it was inherited from the mother or the father.

POSTTRANSCRIPTIONAL CONTROLS

In principle, every step required for the process of gene expression could be controlled. Indeed, one can find examples of each type of regulation, although any one gene is likely to use only a few of them. Controls on the initiation of gene transcription are the predominant form of regulation for most genes. But other controls can act later in the pathway from DNA to protein to modulate the amount of gene product that is made. Although these posttranscriptional controls, which operate after RNA polymerase has bound to the gene's promoter and begun RNA synthesis, are less common than *transcriptional control*, for many genes they are crucial.

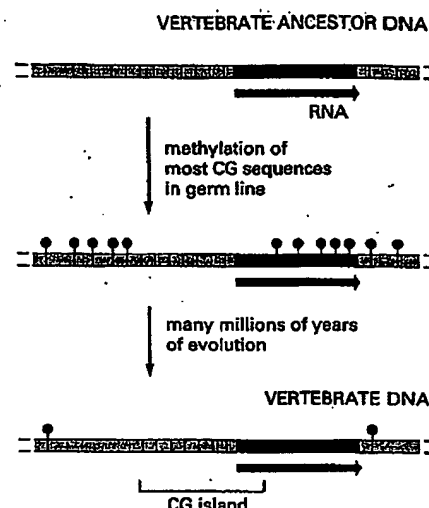


Figure 7-86 A mechanism to explain both the marked overall deficiency of CG sequences and their clustering into CG islands in vertebrate genomes. A black line marks the location of a CG dinucleotide in the DNA sequence, while a red "lollipop" indicates the presence of a methyl group on the CG dinucleotide. CG sequences that lie in regulatory sequences of genes that are transcribed in germ cells are unmethylated and therefore tend to be retained in evolution. Methylated CG sequences, on the other hand, tend to be lost through deamination of 5-methyl C to T, unless the CG sequence is critical for survival.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Ashkenazi et al.

App. No. : 09/903,925

Filed : July 11, 2001

For : SECRETED AND
TRANSMEMBRANE
POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

Examiner : Hamud, Fozia M

Group Art Unit 1647

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DECLARATION OF AVI ASHKENAZI, Ph.D UNDER 37 C.F.R. § 1.132

I, Avi Ashkenazi, Ph.D. declare and say as follows: -

1. I am Director and Staff Scientist at the Molecular Oncology Department of Genentech, Inc., South San Francisco, CA 94080.
2. I joined Genentech in 1988 as a postdoctoral fellow. Since then, I have investigated a variety of cellular signal transduction mechanisms, including apoptosis, and have developed technologies to modulate such mechanisms as a means of therapeutic intervention in cancer and autoimmune disease. I am currently involved in the investigation of a series of secreted proteins over-expressed in tumors, with the aim to identify useful targets for the development of therapeutic antibodies for cancer treatment.
3. My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).
4. Gene amplification is a process in which chromosomes undergo changes to contain multiple copies of certain genes that normally exist as a single copy, and is an important factor in the pathophysiology of cancer. Amplification of certain genes (e.g., Myc or Her2/Neu)

gives cancer cells a growth or survival advantage relative to normal cells, and might also provide a mechanism of tumor cell resistance to chemotherapy or radiotherapy.

5. If gene amplification results in over-expression of the mRNA and the corresponding gene product, then it identifies that gene product as a promising target for cancer therapy, for example by the therapeutic antibody approach. Even in the absence of over-expression of the gene product, amplification of a cancer marker gene - as detected, for example, by the reverse transcriptase TaqMan[®] PCR or the fluorescence *in situ* hybridization (FISH) assays - is useful in the diagnosis or classification of cancer, or in predicting or monitoring the efficacy of cancer therapy. An increase in gene copy number can result not only from intrachromosomal changes but also from chromosomal aneuploidy. It is important to understand that detection of gene amplification can be used for cancer diagnosis even if the determination includes measurement of chromosomal aneuploidy. Indeed, as long as a significant difference relative to normal tissue is detected, it is irrelevant if the signal originates from an increase in the number of gene copies per chromosome and/or an abnormal number of chromosomes.

6. I understand that according to the Patent Office, absent data demonstrating that the increased copy number of a gene in certain types of cancer leads to increased expression of its product, gene amplification data are insufficient to provide substantial utility or well established utility for the gene product (the encoded polypeptide), or an antibody specifically binding the encoded polypeptide. However, even when amplification of a cancer marker gene does not result in significant over-expression of the corresponding gene product, this very absence of gene product over-expression still provides significant information for cancer diagnosis and treatment. Thus, if over-expression of the gene product does not parallel gene amplification in certain tumor types but does so in others, then parallel monitoring of gene amplification and gene product over-expression enables more accurate tumor classification and hence better determination of suitable therapy. In addition, absence of over-expression is crucial information for the practicing clinician. If a gene is amplified but the corresponding gene product is not over-expressed, the clinician accordingly will decide not to treat a patient with agents that target that gene product.

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so

made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By: Avi Ashkenazi
Avi Ashkenazi, Ph.D.

Date: 9/15/03

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CURRICULUM VITAE

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July 2003

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Editorial:

Editorial Board Member: Current Biology

Associate Editor, Clinical Cancer Research.

Associate Editor, Cancer Biology and Therapy.

Refereed papers:

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TECHNICAL UPDATE

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HER-2/neu Breast Cancer Predictive Testing

Julie Sanford Hanna, Ph.D. and Dan Mornin, M.D.

EACH YEAR, OVER 182,000 WOMEN in the United States are diagnosed with breast cancer, and approximately 45,000 die of the disease.¹ Incidence appears to be increasing in the United States at a rate of roughly 2% per year. The reasons for the increase are unclear, but non-genetic risk factors appear to play a large role.²

Five-year survival rates range from approximately 65%-85%, depending on demographic group, with a significant percentage of women experiencing recurrence of their cancer within 10 years of diagnosis. One of the factors most predictive for recurrence once a diagnosis of breast cancer has been made is the number of axillary lymph nodes to which tumor has metastasized. Most node-positive women are given adjuvant therapy, which increases their survival. However, 20%-30% of patients without axillary node involvement also develop recurrent disease, and the difficulty lies in how to identify this high-risk subset of patients. These patients could benefit from increased surveillance, early intervention, and treatment.

Prognostic markers currently used in breast cancer recurrence prediction include tumor size, histological grade, steroid hormone receptor status, DNA ploidy, proliferative index, and cathepsin D status. Expression of growth factor receptors and over-expression of the HER-2/neu oncogene have also been identified as having value regarding treatment regimen and prognosis.

HER-2/neu (also known as c-erbB2) is an oncogene that encodes a transmembrane glycoprotein that is homologous to, but distinct from, the epidermal growth factor receptor. Numerous studies have indicated that high levels of expression of this protein are associated with rapid tumor growth, certain forms of therapy resistance, and shorter disease-free survival. The gene has been shown to be amplified and/or overexpressed in 10%-30% of invasive breast cancers and in 40%-60% of intraductal breast carcinoma.³

There are two distinct FDA-approved methods by which HER-2/neu status can be evaluated: immunohistochemistry (IHC, HercepTest™) and FISH (fluorescent in situ hybridization, PathVysion™ Kit). Both methods can be performed on archived and current specimens. The first method allows visual assessment of the amount of HER-2/neu protein present on the cell membrane. The latter method allows direct quantification of the level of gene amplification present in the tumor, enabling differentiation between low- versus high-amplification. At least one study has demonstrated a difference in

recurrence risk in women younger than 40 years of age for low- versus high-amplified tumors (54.5% compared to 85.7%); this is compared to a recurrence rate of 16.7% for patients with no HER-2/neu gene amplification.⁴ HER-2/neu status may be particularly important to establish in women with small (≤ 1 cm) tumor size.

The choice of methodology for determination of HER-2/neu status depends in part on the clinical setting. FDA approval for the Vysis FISH test was granted based on clinical trials involving 1549 node-positive patients. Patients received one of three different treatments consisting of different doses of cyclophosphamide, Adriamycin, and 5-fluorouracil (CAF). The study showed that patients with amplified HER-2/neu benefited from treatment with higher doses of adriamycin-based therapy, while those with normal HER-2/neu levels did not. The study therefore identified a sub-set of women, who because they did not benefit from more aggressive treatment, did not need to be exposed to the associated side effects. In addition, other evidence indicates that HER-2/neu amplification in node-negative patients can be used as an independent prognostic indicator for early recurrence, recurrent disease at any time and disease-related death.⁵ Demonstration of HER-2/neu gene amplification by FISH has also been shown to be of value in predicting response to chemotherapy in stage-2 breast cancer patients.

Selection of patients for Herceptin® (Trastuzumab) monoclonal antibody therapy, however, is based upon demonstration of HER-2/neu protein overexpression using HercepTest™. Studies using Herceptin® in patients with metastatic breast cancer show an increase in time to disease progression, increased response rate to chemotherapeutic agents and a small increase in overall survival rate. The FISH assays have not yet been approved for this purpose, and studies looking at response to Herceptin® in patients with or without gene amplification status determined by FISH are in progress.

In general, FISH and IHC results correlate well. However, subsets of tumors are found which show discordant results; i.e., protein overexpression without gene amplification or lack of protein overexpression with gene amplification. The clinical significance of such results is unclear. Based on the above considerations, HER-2/neu testing at SHMC/PAML will utilize immunohistochemistry (HercepTest®) as a screen, followed by FISH in IHC-negative cases. Alternatively, either method may be ordered individually depending on the clinical setting or clinician preference.

CPT code information

HER-2/neu via IHC

88342 (including interpretive report)

HER-2/neu via FISH

88271x2 Molecular cytogenetics, DNA probe, each

88274 Molecular cytogenetics, interphase in situ hybridization, analyze 25-99 cells

88291 Cytogenetics and molecular cytogenetics, interpretation and report

Procedural Information

Immunohistochemistry is performed using the FDA-approved DAKO antibody kit, Herceptest[®]. The DAKO kit contains reagents required to complete a two-step immunohistochemical staining procedure for routinely processed, paraffin-embedded specimens. Following incubation with the primary rabbit antibody to human HER-2/neu protein, the kit employs a ready-to-use dextran-based visualization reagent. This reagent consists of both secondary goat anti-rabbit antibody molecules with horseradish peroxidase molecules linked to a common dextran polymer backbone, thus eliminating the need for sequential application of link antibody and peroxidase conjugated antibody. Enzymatic conversion of the subsequently added chromogen results in formation of visible reaction product at the antigen site. The specimen is then counterstained; a pathologist using light-microscopy interprets results.

FISH analysis at SHMC/PAML is performed using the FDA-approved PathVysion[™] HER-2/neu DNA probe kit, produced by Vysis, Inc. Formalin fixed, paraffin-embedded breast tissue is processed using routine histological methods, and then slides are treated to allow hybridization of DNA probes to the nuclei present in the tissue section. The PathVysion[™] kit contains two direct-labeled DNA probes, one specific for the alphoid repetitive DNA (CEP 17, spectrum orange) present at the chromosome 17 centromere and the second for the HER-2/neu oncogene located at 17q11.2-12 (spectrum green). Enumeration of the probes allows a ratio of the number of copies of chromosome 17 to the number of copies of HER-2/neu to be obtained; this enables quantification of low versus high amplification levels, and allows an estimate of the percentage of cells with HER-2/neu gene amplification. The clinically relevant distinction is whether the gene amplification is due to increased gene copy number on the two chromosome 17 homologues normally present or an increase in the number of chromosome 17s in the cells. In the majority of cases, ratio equivalents less than 2.0 are indicative of a normal/negative result, ratios of 2.1 and over indicate that amplification is present and to what degree. Interpretation of this data will be performed and reported from the Vysis-certified Cytogenetics laboratory at SHMC.

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MOLECULAR BIOLOGY OF THE CELL

**Bruce Alberts • Dennis Bray
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The ribosomes of the rough ER are held on the membrane in part by their growing polypeptide chains, which are threaded across the ER membrane as they are synthesized (see below). However, when the synthesis of polypeptide chains is terminated with a drug like puromycin, these ribosomes still remain tightly bound to the membrane of rough microsomes. Such ribosomes can be dislodged by suspending the microsomes in a solution of high salt concentration, which breaks the interactions between the ribosomes and special membrane proteins of the rough microsomes. Furthermore, ribosomes can reassociate with rough microsomal membranes from which ribosomes have been removed. They bind rapidly and with a high affinity to a limited number of sites on the membrane, so that the "stripped" membrane will regain the same number of ribosomes it had when originally isolated.

The binding site on the ribosome is located on the large subunit and seems to attach to two specific glycoproteins in the rough ER membrane. These two proteins, called *ribophorins*, span the ER membrane, and they are found exclusively in the rough regions of ER. It is not clear how the ribophorins are prevented from diffusing into the membrane of the smooth ER. They could be segregated by forming large two-dimensional crystals in the bilayer, or they could be tethered in place by fibrous proteins on either side of the bilayer (see p. 283). Whatever the mechanism, it probably accounts for the flattened appearance of the rough ER in comparison with that of the smooth ER.

Membrane-bound Ribosomes Synthesize Proteins That Pass Through the Membrane During Their Translation¹⁷

Many proteins at some stage must cross the permeability barrier presented by a cell membrane. Proteins secreted from the cell (secretory proteins) are the most obvious of numerous examples. In this case, the binding of the ribosomes to the membrane of the ER helps to solve the problem of getting these water-soluble proteins across a hydrophobic membrane: the proteins thread their way across the ER membrane as they are synthesized before they have had a chance to fold into their final hydrophilic conformations. Once inside the lumen of the rough ER, the proteins to be secreted are transported through the Golgi apparatus and then to the outside of the cell. Thus, secretory proteins become permanently segregated from the cytosol as soon as they have been synthesized.

A similar but more subtle problem is presented by membrane proteins destined to span the lipid bilayer. Often, large hydrophilic portions of these polypeptide chains end up being exposed on the luminal side of intracellular membranes or on the topologically equivalent extracellular side of the plasma membrane (Figure 7-26). Unlike secreted proteins, membrane proteins are not made in large amounts, so their mode of synthesis is more difficult to study.

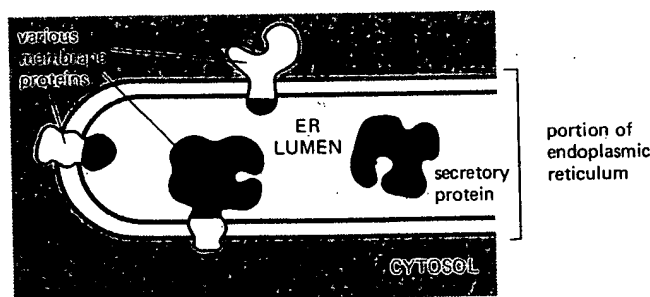


Figure 7-26 Schematic diagram of four different proteins, emphasizing the portion of each protein that has passed through the lipid bilayer of the ER during protein synthesis. Three different membrane proteins and a secretory protein are shown. The colored region of each has passed through the bilayer.

However, one membrane protein produced in large amounts by cells is the G protein of the enveloped *vesicular stomatitis virus* (VSV). When this virus infects a cell, only one membrane protein, the G protein, is made by the cell, instead of the hundreds or thousands of different kinds that are synthesized in uninfected cells. This makes it relatively easy to follow its synthesis. It has been shown that most of the G-protein polypeptide chain is transferred across the ER membrane as it is synthesized, just as in the case of a secreted protein. However, instead of being released into the lumen of the ER, the protein remains anchored in the bilayer by a short hydrophobic segment of the polypeptide chain. The G protein thereby remains membrane-bound; the 500 amino acids that have crossed the ER membrane will form an external "spike," which protudes from the lipid bilayer coating the final virus particle.

Membrane-bound ribosomes whose translation products cross the ER membrane during synthesis are said to be engaged in **vectorial discharge**. This term is useful because it emphasizes two important features of the process. First, the ribosome is found only on the cytosolic side of the ER membrane, so that the transfer of the polypeptide chain across the membrane must be "vectorial," in the direction from cytosol to lumen. (Transfer is also vectorial in the sense that the polypeptide is passed with its amino-terminal end first, since this is the direction of protein synthesis [p. 206].) Second, the term "discharge" emphasizes that this must be an active, energy-requiring process. The mechanism that permits the growing polypeptide to cross the membrane is still unknown, as is the source of the required energy, but these issues can now be approached biochemically using cell-free systems. It is possible that a novel sort of transport protein, such as an energy-requiring polypeptide pump, is involved in vectorial discharge.

Direct Evidence Favoring Vectorial Discharge Has Come from Experiments in Bacteria¹⁸

The concept of vectorial discharge derives from experiments first performed in 1966 showing that many of the nascent polypeptides released from microsomes by puromycin remain sequestered in the microsome lumen. But the most convincing experiments were not done until 1977, and, as is so often the case, they involved bacterial cells. Gram-positive bacteria, such as *Bacillus subtilis*, secrete large quantities of enzymes. There being no ER in bacteria, these enzymes are synthesized by ribosomes bound to the plasma membrane. In the experiment illustrated in Figure 7-27, it was found that one end of these secreted polypeptide chains could be selectively hydrolyzed by proteolytic enzymes added to intact bacterial cells whose cell walls had been removed, while the other end, which was still being synthesized by ribosomes inside the cell, could not be hydrolyzed. This showed that one end of the growing polypeptide chain must be exposed on the outside of the cell. Moreover, almost all of the completed portion of a nascent polypeptide was attacked by the protease, leaving only a small undigested segment 50 amino acid residues long. Since a resistant segment of about 30 amino acid residues is left within the ribosome when free ribosomes are subjected to mild proteolysis, these observations suggest that only about 20 residues of each polypeptide are within the membrane at any one time during vectorial discharge. This length of polypeptide is sufficient to cross the lipid bilayer just once.

Although it has been attempted, this type of experiment cannot be done as convincingly with eucaryotic rough microsomes. The main problem is that the topology is backward; the growing polypeptide is sequestered inside the microsome, and there is at present no way of restricting the action of an added protease exclusively to the microsome interior.

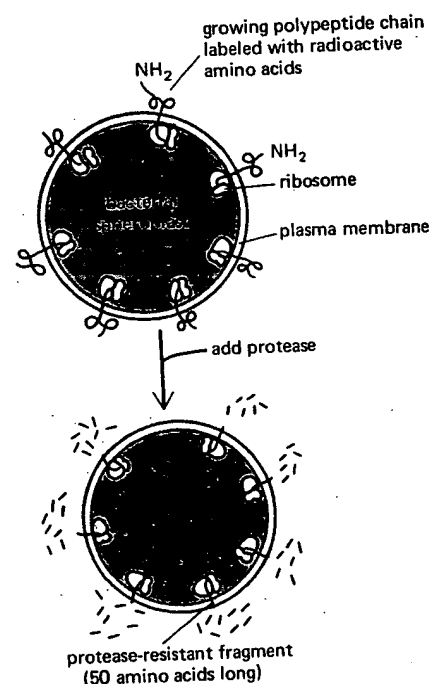


Figure 7-27 Schematic illustration of vectorial transport in bacteria. After the cell walls have been removed (to form spheroplasts), the cells are briefly exposed to radioactive amino acids to label the growing polypeptide chains synthesized by plasma-membrane-bound ribosomes. Part of the growing polypeptide chain has been transferred across the membrane and can be digested by the protease treatment. The drawing is not to scale; in reality the diameter of the ribosome is only about one-fortieth of the diameter of the bacterial cell.

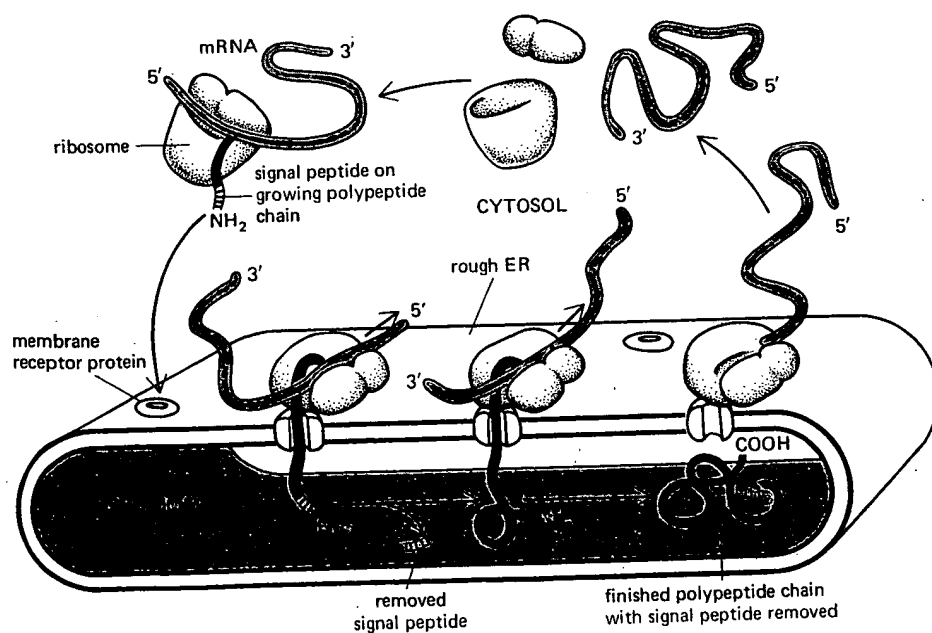
Membrane-bound Ribosomes Are Derived from Free Ribosomes That Are Directed to the ER Membrane by Special Signal Sequences¹⁹

Although the membrane-bound ribosomes of the rough ER synthesize a selected class of proteins destined for vectorial discharge, there is no evidence that the ribosomes themselves differ from those free in the cytoplasm. In the current view, membrane-bound ribosomes are simply ribosomes that are specifically directed to the ER membrane because of the polypeptide chain they happen to be translating.

An important insight into how ribosomes are directed to the ER came from detailed studies of antibody (immunoglobulin) synthesis. The light and heavy chains of immunoglobulin constitute the principal secretory products of the plasma cells of the immune system (Chapter 17). When mRNA encoding the light chain of an immunoglobulin is translated *in vitro* by free ribosomes, the light chain is synthesized in the form of a precursor containing an extra 20 amino acid residues not found in the secreted product. The extra "leader" peptide is located at the extreme amino terminus of the precursor immunoglobulin. But chains synthesized *in vitro* by ribosomes attached to rough microsomes lack this extra amino-terminal peptide. These discoveries provided evidence for an earlier proposal that the *leader sequence* peptide acts as a "signal" to direct the ribosome to the rough regions of the ER membrane (Figure 7-28). Some receptor that recognizes proteins containing this *signal peptide* must therefore be present exclusively in the rough regions of the ER membrane.

This viewpoint has been greatly fortified by the subsequent discovery that the major secretory proteins of the pancreas, when synthesized *in vitro* on free ribosomes, are translated as precursor polypeptides ("presecretory" proteins) containing a similar amino-terminal leader sequence of 16 residues not found *in vivo*. Since then, precursors to dozens of secretory and integral membrane proteins in procaryotes and eucaryotes have been described. In all of these cases, the amino-terminal **signal sequence** contains large numbers of hydrophobic amino acid residues, even though the actual sequences

Figure 7-28 A schematic view of the signal peptide hypothesis. For simplicity, only a single ribosome, rather than a polyribosome, is shown. The indicated binding of a cytosolic ribosome to the rough ER is now thought to require two separate interactions: an affinity of the ribosome itself for special membrane proteins in the ER (presumably the ribophorins, see p. 341) and the interaction of an amino-terminal signal peptide on the growing polypeptide chain with a membrane receptor protein. However, once protein transfer across the membrane begins, the growing polypeptide chain itself helps to anchor the ribosome, replacing the second interaction.



are quite variable. It has now been shown that these signal sequences are, in fact, removed on the luminal side of the rough ER, even before the synthesis of the polypeptide is completed, by a specific protease found only in rough microsomes. This type of amino-terminal sequence that is cleaved off after protein synthesis has never been found on a protein that remains in the cytosol.

Ribosomes in the cytosol that begin synthesizing a protein destined for the ER must be brought to the rough ER to begin the vectorial discharge process. But how are these ribosomes specifically recognized by the ER membrane? Recent evidence has shown that a multisubunit protein present in the cytosol binds to these ribosomes shortly after they have synthesized the appropriate signal peptide. This protein, called *signal recognition protein*, halts further protein synthesis by the ribosome until it has become linked to the rough ER membrane. Presumably, this protein recognizes both the amino terminus of the newly synthesized protein and some receptor on the rough ER membrane, thereby binding the ribosome to the ER. Protein synthesis by the ribosome then resumes, as vectorial discharge begins. While the nature of the receptor in the ER membrane is unknown, the ribophorins are thought to be involved in stabilizing the ribosome-ER complex.

There Is Genetic Evidence for the Signal Hypothesis²⁰

Genetic analysis of procaryotes has been used in two different ways to test the idea that leader sequences act as the proposed signals for the vectorial discharge of proteins. (1) Many mutants of an *E. coli* membrane protein have been isolated in which the protein is retained in the cytoplasm instead of being inserted in the membrane. Most of these mutations have been found to alter the extreme amino-terminal leader sequence region of the protein. (2) In specially designed strains of *E. coli*, the DNA segments coding for polypeptide chains of integral membrane proteins and of cytosolic proteins have been fused to create new hybrid proteins. When a substantial length of the amino-terminal portion of a membrane protein of *E. coli* is fused with most of the carboxyl-terminal portion of a cytosolic protein, the hybrid protein is found in the membrane. Thus, only the amino-terminal portion seems to be required for passage into a membrane.

Experiments in *E. coli* using hybrid proteins have demonstrated another important fact about signal sequences: although these sequences are required for directing the growing polypeptide to the membrane, they are not always sufficient in themselves. A hybrid protein containing only a very short length of the amino terminus of a membrane protein—including all of its leader sequence—was not inserted into the membrane. Thus, the leader sequence may normally interact with neighboring regions of the polypeptide chain to create a unique three-dimensional arrangement of amino acids, and it is this arrangement—rather than the leader sequence itself—that is required for specific membrane insertion.

Some Proteins Cross Membranes by a Posttranslational Import Mechanism Rather Than by Vectorial Discharge²¹

Some proteins can cross certain membranes long after their synthesis on ribosomes. For example, most of the proteins inside mitochondria and chloroplasts are coded for by nuclear genes (Chapter 9). These proteins are synthesized and released in the cytosol and then are pumped across the appropriate organelle membrane in an energy-requiring process (**posttranslational import**). Interestingly, most of these imported proteins also contain amino-terminal leader sequences that are removed following transport across the mitochondrial or chloroplast membranes. These leader sequences have been

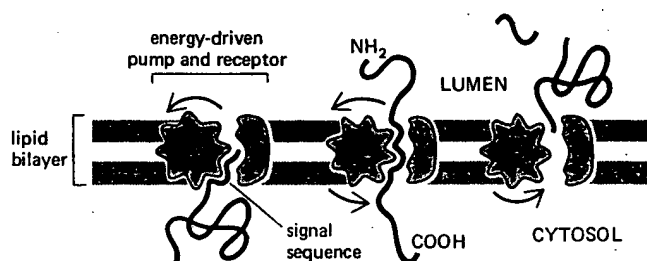


Figure 7-29 Schematic view of an energy-driven protein pump. After a receptor recognizes some special feature of an amino-terminal peptide, the pump is activated to force the entire protein through the membrane. A mechanism of this type is apparently needed to account for the observed transfer of already synthesized proteins from the cytosol into mitochondria and chloroplasts.

shown to be required to provide the "signal" that is recognized to direct the protein to the correct site. The membranes of both of these cellular organelles must contain a specific receptor for the appropriate amino-terminal signal. These receptors would seem to be functionally linked to an energy-driven pump that forces the recognized protein across the membrane, possibly unfolding it transiently in the process (Figure 7-29).

Some membrane proteins may enter and partially cross the ER membrane by a posttranslational import mechanism. This is probably the case for proteins that have a large amount of their mass in the lipid bilayer and only small portions exposed on the noncytoplasmic side of the membrane. It is easy to imagine how such a hydrophobic membrane protein could simply dissolve in the lipid bilayer after being released into the cytosol or even during its synthesis. The energy required to transfer a relatively small hydrophilic portion of the protein across the lipid bilayer could come from the gain in free energy associated with the transfer of the hydrophobic portion from an aqueous environment to the hydrophobic interior of the bilayer. Some of the proteins located in the outer membrane of mitochondria appear to enter their membrane in this way following their synthesis on ribosomes in the cytosol (see p. 539).

Even if we consider only the few examples just discussed, it is obvious that many different types of signal sequences must exist on proteins. Some signals will direct a protein to the ER, others to a mitochondrion, and yet others to a chloroplast (in a plant cell). The recognition systems involved must have a high degree of selectivity, since proteins seem to be directed quite reliably to their correct intracellular address.

Most Proteins Synthesized in the Rough ER Are Glycosylated²²

Glycosylation is one of the major biosynthetic functions of the ER. It is a striking fact that most proteins sequestered in the lumen of the ER before being secreted from the cell or transported to other intracellular destinations (such as the Golgi apparatus, lysosomes, or plasma membrane) are **glycoproteins** (Figure 7-30). In contrast, the soluble proteins of the cytosol are not glycosylated.

An important advance in understanding the process of glycosylation was the discovery that mainly one species of oligosaccharide (composed of *N*-acetylglucosamine, mannose, and glucose) is transferred to proteins in the ER, and that this oligosaccharide is always linked to the NH_2 group on the side chain of an asparagine residue of the protein (Figure 7-31). All of the diversity of the asparagine-linked oligosaccharide structures on mature glycoproteins results from extensive modifications of this single precursor structure, most of which occur during subsequent transit through the Golgi apparatus (p. 357). The asparagine-linked oligosaccharides (***N*-linked oligosaccharides**) are by far the most common ones found in glycoproteins. Often, but less frequently, oligosaccharides are linked to the OH group on the side

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